

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 17:27:07 ; Search time 189 Seconds
 (without alignments)
 24.4.099 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLVYVSDCA.....CSRFPDGGRYRCSDMLKNINP 105

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A. Geneseq 21: *
 1: geneseq1980s: *
 2: geneseq1990s: *
 3: geneseq2000s: *
 4: geneseq2001s: *
 5: geneseq2002s: *
 6: geneseq2003s: *
 7: geneseq2004s: *
 8: geneseq2005s: *
 9: geneseq2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-------------|--|
| 1 | 589 | 100.0 | 105 | 3 RAY66745 | Aay66745 Membrane- Aab18453 A human T |
| 2 | 589 | 100.0 | 105 | 3 AAB18453 | Aab70148 Human G_P |
| 3 | 589 | 100.0 | 105 | 4 AAB68427 | Aab68427 Amino_acid |
| 4 | 589 | 100.0 | 105 | 4 AAB12406 | Aab12406 Human PRO |
| 5 | 589 | 100.0 | 105 | 4 AAB53096 | Aab53096 Human ang |
| 6 | 589 | 100.0 | 105 | 4 AAB5268 | Aab6528 Human PRO |
| 7 | 589 | 100.0 | 105 | 4 AAB49175 | Aab48175 Human PRO |
| 8 | 589 | 100.0 | 105 | 4 AAB4867 | Aab4867 Human ext |
| 9 | 589 | 100.0 | 105 | 5 AAM5073 | Aam5073 Endocrine |
| 10 | 589 | 100.0 | 105 | 5 AAB08674 | Aab08674 Human PRO |
| 11 | 589 | 100.0 | 105 | 5 AAB4902 | Aab84902 Human PRO |
| 12 | 589 | 100.0 | 105 | 5 AAO15527 | Aao15527 Human phy |
| 13 | 589 | 100.0 | 105 | 5 ABB00308 | Abb66308 Human G_P |
| 14 | 589 | 100.0 | 105 | 5 AAE24382 | Aae24382 Human pro |
| 15 | 589 | 100.0 | 105 | 5 ABB5508 | Abb5508 Human ang |
| 16 | 589 | 100.0 | 105 | 5 ADY31906 | Ady31906 Novel hum |
| 17 | 589 | 100.0 | 105 | 6 ABB0803 | Abi5803 Human PRO |
| 18 | 589 | 100.0 | 105 | 6 ABB59161 | Abi59161 Novel hum |
| 19 | 589 | 100.0 | 105 | 6 ABB2673 | Abi2673 Human sec |
| 20 | 589 | 100.0 | 105 | 6 ABB017850 | Abi017850 Novel hum |
| 21 | 589 | 100.0 | 105 | 6 ABB06592 | Abi60592 Human sec |
| 22 | 589 | 100.0 | 105 | 6 ABB0821 | Abi08021 Human PRO |
| 23 | 589 | 100.0 | 105 | 6 ABB033787 | Abi033787 Novel hum |
| 24 | 589 | 100.0 | 105 | 6 ABB033787 | Abi033787 Novel hum |

| Score | Length | DB ID | Description | Accession | Organism | Protein | Function |
|-------|--------|-------|-------------|------------|--------------------|---------|----------|
| 25 | 589 | 100.0 | 105 | 6 ABU13974 | Abu13974 Human PRO | | |
| 26 | 589 | 100.0 | 105 | 6 ABU08800 | Abu08800 Human end | | |
| 27 | 589 | 100.0 | 105 | 6 ABU81104 | Abu81104 Human PRO | | |
| 28 | 589 | 100.0 | 105 | 6 ABU07603 | Abu07603 Human ZPE | | |
| 29 | 589 | 100.0 | 105 | 6 ABU72559 | Abu72559 Novel hum | | |
| 30 | 589 | 100.0 | 105 | 6 ABU66804 | Abu66804 Human PRO | | |
| 31 | 589 | 100.0 | 105 | 6 ABU59885 | Abu59885 Novel sec | | |
| 32 | 589 | 100.0 | 105 | 6 ABU59308 | Abu59308 Human sec | | |
| 33 | 589 | 100.0 | 105 | 6 AB026005 | Ab026005 Human PRO | | |
| 34 | 589 | 100.0 | 105 | 6 AB025075 | Abc25075 Human sec | | |
| 35 | 589 | 100.0 | 105 | 6 ABU82130 | Abu82130 Novel hum | | |
| 36 | 589 | 100.0 | 105 | 6 ABU59014 | Abu59014 Human sec | | |
| 37 | 589 | 100.0 | 105 | 6 ABU92392 | Abu92392 Novel hum | | |
| 38 | 589 | 100.0 | 105 | 6 ABU59457 | Abu59457 Novel hum | | |
| 39 | 589 | 100.0 | 105 | 6 ABU67080 | Abu67080 Human sec | | |
| 40 | 589 | 100.0 | 105 | 6 ABU92223 | Abu92223 Novel hum | | |
| 41 | 589 | 100.0 | 105 | 6 ABU10929 | Abu10929 Human PRO | | |
| 42 | 589 | 100.0 | 105 | 6 ABU81681 | Abu81681 Novel hum | | |
| 43 | 589 | 100.0 | 105 | 6 ABU88620 | Abu88620 Human sec | | |
| 44 | 589 | 100.0 | 105 | 6 AB034134 | Ab034134 Human PRO | | |
| 45 | 589 | 100.0 | 105 | 6 ADA45989 | Ada45989 Novel hum | | |

ALIGNMENTS

PR 10-JUN-1998; 98US-0088825P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 15-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089601P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
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 PR 23-JUN-1998; 98US-0090349P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090431P.
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 PR 24-JUN-1998; 98US-0090472P.
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 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 25-JUN-1998; 98US-0090682P.
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 PR 01-JUL-1998; 98US-0091358P.
 PR 02-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-009242P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
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 PR 04-AUG-1998; 98US-0095325P.

PR 10-AUG-1998; 98US-0095916P.
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 PR 10-AUG-1998; 98US-0096012P.
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 PR 12-AUG-1998; 98US-0096229P.
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 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
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 PR 19-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
 PR 24-AUG-1998; 98US-0097561P.
 PR 26-AUG-1998; 98US-0097931P.
 PR 26-AUG-1998; 98US-0097932P.
 PR 18-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097992P.
 PR 26-AUG-1998; 98US-0097995P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098535P.
 PR 16-SEP-1998; 98US-0100344P.
 PR 12-JAN-1999; 99US-0115565P.

XX (GBTM) GENENTECH INC.
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
 PI Wood WI, Yuan J,
 XX DR WPI; 2000-072883/06.
 XX N-PSDB; AA265091.

PT Membrane-bound proteins and related nucleotide sequences.
 XX
 PS Claim 12; Fig 266; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including TLR receptors, TIR ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunodhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

XX Sequence 105 AA;

Query Match 100.0%; Score 589; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 MRCATRIVSMLIIVTSDCAVITGACRDRDVCGAGTCCTAISLWLRGLMCTRLGRGEGBC 60

Db 1 MRGATRVSIMLLVVSPCAVITGACERDVQGAGTCACISLWLRGLRMCTPLGREGEEC 60
 QY 61 HPGSHKVPFRKRAKHTCPCCLPNLCSRFPDGRYRCSDMLKNINF 105
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders
 XX SQ Sequence 105 AA;

RESULT 2
 AAB18453
 ID AAB18453 standard; protein; 105 AA.
 XX
 AC AAB18453;
 XX DT 15-JAN-2001 (first entry)
 XX DB A human TANGO 266 polypeptide.
 XX
 TANGO 266; TANGO 216; TANGO 261; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .19
 /note= "signal sequence"
 FT Protein 20. .106
 /note= "mature protein"
 XX WO20052022-A1.
 XX PD 08-SEP-2000.
 XX PR 01-MAR-2000; 2000WO-US005226.
 XX PR 01-MAR-1999; 99US-0122458P.
 XX PA (MILLI-) MILLENNIUM PHARM INC.
 PT Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 DR XX
 DR N-PSDB; AAA75155.
 XX PT Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.
 XX PS Claim 8; Fig 14; 175pp; English.
 XX
 CC The present sequence represents a human TANGO 266 polypeptide. The
 CC specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC Sequence 105 AA;

CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders
 XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 3; Length 105;
 ID Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 105; Conservative 0; MisMatch 0; Indels 0; Gaps 0;
 XX
 QY 1 MRGATRVSIMLLVVSPCAVITGACERDVQGAGTCACISLWLRGLRMCTPLGREGEEC 60
 DB 1 MRGATRVSIMLLVVSPCAVITGACERDVQGAGTCACISLWLRGLRMCTPLGREGEEC 60
 QY 61 HPGSHKVPFRKRAKHTCPCCLPNLCSRFPDGRYRCSDMLKNINF 105
 DB 61 HPGSHKVPFRKRAKHTCPCCLPNLCSRFPDGRYRCSDMLKNINF 105
 XX SQ Sequence 105 AA;

RESULT 3
 AAB70148
 ID AAB70148 standard; protein; 105 AA.
 XX
 AC AAB70148;
 XX DT 29-MAY-2001 (first entry)
 XX DE Human G protein-coupled receptor protein-related sequence #4.
 XX KW Human; G protein-coupled receptor protein; nootropic; neuroprotective;
 KW hypotensive; orexigenic; antiallergic; antiangiogen; antimicrobial;
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
 KW allergy; angina pectoris; infection; MRSA;
 KW multiple resistant Staphylococcus aureus.
 XX OS Homo sapiens.
 XX PN WO200116309-A1.
 XX PD 08-MAR-2001.
 XX PR 24-AUG-2000; 2000WO-JP005685.
 XX PR 27-AUG-1999; 99JP-0024131.
 XX PR 18-JUL-2000; 2000JP-00217474.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PT Watanabe T, Terao Y, Shintani Y;
 DR XX
 DR WPI; 2001-226684/23.
 XX PT New human brain-originated guanosine triphosphate protein-coupled
 PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
 PT and development of preventives and remedies for Alzheimer's disease,
 PT hypertension and anorexia.
 XX PS Example 4; Page 113; 119pp; Japanese.

CC The present sequence is provided in a specification relating to a protein
 CC or its salt with an amino acid sequence identical or substantially
 CC similar to a fully defined sequence of 393 amino acids as given in the
 CC specification. The protein is useful in gene diagnosis and development of
 CC preventives and remedies for disease associated with dysfunction of the
 CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
 CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
 CC aureus. The proteins and DNA encoding the proteins are also useful for
 CC the treatment of these diseases by gene therapy.

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLUVTSDCAVTGACERDVOGAGTCGAISIWRGIRMCPLGREGBC 60
 1 MRGATRVSIMLUVTSDCAVTGACERDVOGAGTCGAISIWRGIRMCPLGREGBC 60

QY 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105
 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105

Db 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105
 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105

RESULT 4

AAB68427
 ID AAB68427 standard; protein; 105 AA.
 XX
 AC AAB68427;
 DT 23-JUL-2001 (first entry)

DE Amino acid sequence of a human zven2 polypeptide.

XX
 KW Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing; antitumour; antiinflammatory; neurosis; tissue growth; digestive enzyme; cellular differentiation; gastrointestinal; cell contractility; gastrointestinal motility; inflammation; hypermotility; diarrhoea; Crohn's disease.

XX
 OS Homo sapiens.
 XX
 PN WO200136465-A2.
 XX
 PD 25-MAY-2001.
 XX
 PR 14-NOV-2000; 2000WO-US031278.
 XX
 PR 16-NOV-1999; 99US-00442164.
 PR 25-FEB-2000; 2000US-00511679.
 PR 19-APR-2000; 2000US-00552203.
 PR 07-JUN-2000; 2000US-0210332P.

XX
 (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Bishop PD, Whitmore TE, Thompson PP;
 XX
 DR WPI; 2001-355611/37.
 DR N-PSDB; AAF5427.

PT Novel isolated zven polypeptide useful for inhibiting proliferation of tumor cells, for treating small cell cancer of lung, to promote wound healing, and for treating Crohn's disease and diarrhea.

PS Claim 27; Page 4; 98pp; English.

XX
 CC The present sequence represents a human Zven2 polypeptide. The specification also describes Zven1. The Zven1 gene is present on chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven polymycotides and polypeptides are useful in veterinary and human therapeutics for treating small cell cancer of the lung, to promote wound healing, to prevent or to treat an adverse reaction of the skin to a skin-sensitizing agent or a skin-irritating agent, to stimulate the immune system of an immunocompromised individual, as antitumour agents, as antiinflammatory agents, as agents to regulate regeneration or remodeling of tissue, as agents to modulate necrosis or tissue growth developmental arrest, to inhibit proliferation of tumour cells, cellular differentiation and necrosis, to treat disorders associated with gastrointestinal cell contraction, secretion of digestive enzymes and acids, gastrointestinal motility, recruitment of digestive enzymes, inflammation, and conditions associated with hypermotility such as diarrhea and Crohn's disease

RESULT 5

AAU12405
 ID AAU12405 standard; protein; 105 AA.
 XX
 AC AAU12405;
 DT 24-OCT-2001 (first entry)

DE Human PRO186 polypeptide sequence.

XX
 KW human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIa; gene therapy.

XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PR 01-DEC-2000; 2000WO-US032678.
 XX
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 03-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 03-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000319.
 PR 06-JAN-2000; 2000WO-US000377.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US003411.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005014.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-018702P.
 PR 10-MAR-2000; 2000US-018703P.
 PR 15-MAR-2000; 2000WO-US005884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.

SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLUVTSDCAVTGACERDVOGAGTCGAISIWRGIRMCPLGREGBC 60
 1 MRGATRVSIMLUVTSDCAVTGACERDVOGAGTCGAISIWRGIRMCPLGREGBC 60

QY 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105
 61 HPGSHKVPFFRKRIGHTCPCLPNLCSRFPDGRYRCSDMLKINF 105

| SQ | Sequence 105 AA; | PT | PRO polynucleotides used to produce polypeptides used to target bioactive |
|----|--|--------------------------------------|--|
| | 100.0%; Score 589; DB 4; Length 105; | PT | molecules such as toxins, radiolabels or antibodies, to specific cells, |
| | Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0; | PT | to cause targeted cell death. |
| | Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | XX | |
| QY | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 | XX | Claim 12; FIG 266; 935pp; English. |
| Db | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 | CC | The present invention describes human secreted and transmembrane PRO |
| QY | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 | CC | proteins. The PRO proteins have cytostatic activity. The PRO proteins can |
| Db | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 | CC | be used for targeted delivery of bioactive molecules, such as toxins, |
| | | CC | radiolabels or antibodies, that cause cell death. PRO nucleotide |
| | | CC | sequences, and their fragments, that can be used as hybridisation probes, in |
| | | CC | chromosomal and gene mapping, and in the generation of anti-sense RNA and |
| | | CC | DNA. They may also be used to produce transgenic animals which are used |
| | | CC | to develop and screen therapeutically useful reagents. The PRO nucleotide |
| | | CC | and protein sequence can be used for tissue typing and in treating |
| | | CC | cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4470 to |
| | | CC | AAF4470 represent PCR primers and hybridisation probes used in the |
| | | CC | isolation of human PRO Sequences. AAF4470 to AAF4479 and AAF45154 to |
| | | CC | AAF45300 represent human PRO polynucleotide and protein Sequences given |
| | | XX | in the exemplification of the present invention |
| SQ | Sequence 105 AA; | PT | |
| DE | Human PRO1186 (UNP600) protein sequence SEQ ID NO:371. | Query Match | |
| XX | | 100.0%; Score 589; DB 4; Length 105; | |
| KW | Human; secreted and transmembrane protein; PRO; cytostatic; cell death; | Best Local Similarity | 100.0%; Pred. No. 3.8e-54; |
| KW | cancer; chromosomal mapping; gene mapping; tissue typing; | Mismatches | 0; Mismatches 0; |
| KW | diagnostic assay. | Indels | 0; Indels 0; |
| OS | Homo sapiens. | Gaps | 0; Gaps 0; |
| XX | | Matches | 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| PN | WO200073454-A1. | QY | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| PD | 07-DEC-2000. | Db | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| XX | | QY | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| PF | 30-MAR-2000; 2000WO-US008439. | Db | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| XX | | | |
| PR | 02-JUN-1999; 99WO-US012252. | RESULT 8 | |
| PR | 23-JUN-1999; 99US-0141037P. | PR | 100.0%; Score 589; DB 4; Length 105; |
| PR | 07-JUL-1999; 99US-0143048P. | PT | Best Local Similarity 100.0%; Pred. No. 3.8e-54; |
| PR | 20-JUL-1999; 99US-0144758P. | Matches | 0; Mismatches 0; |
| PR | 26-JUL-1999; 99US-0145698P. | Indels | 0; Indels 0; |
| PR | 11-AUG-1999; 99US-0149396P. | Gaps | 0; Gaps 0; |
| PR | 15-SEP-1999; 99WO-US021090. | Matches | 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| PR | 15-SEP-1999; 99WO-US021547. | QY | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| PR | 08-OCT-1999; 99US-0158663P. | Db | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| PR | 30-NOV-1999; 99WO-US028313. | QY | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| PR | 01-DEC-1999; 99WO-US028301. | Db | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| PR | 16-DEC-1999; 99WO-US030095. | | |
| PR | 20-DEC-1999; 99WO-US030911. | RESULT 8 | |
| PR | 05-JAN-2000; 2000WO-US000376. | PR | 100.0%; Score 589; DB 4; Length 105; |
| PR | 06-JAN-2000; 2000WO-US000376. | PT | Best Local Similarity 100.0%; Pred. No. 3.8e-54; |
| PR | 11-FEB-2000; 2000WO-US003565. | Matches | 0; Mismatches 0; |
| PR | 18-FEB-2000; 2000WO-US004341. | Indels | 0; Indels 0; |
| PR | 22-FEB-2000; 2000WO-US004414. | Gaps | 0; Gaps 0; |
| PR | 24-FEB-2000; 2000WO-US004914. | Matches | 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| PR | 02-MAR-2000; 2000WO-US005004. | QY | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| PR | 15-MAR-2000; 2000WO-US006884. | Db | 1 MRGATRISIMLLIVTSDCAVTGACERDVQCGAGTCAILSRGLRMCPIGLGREBEC 60 |
| PR | 20-MAR-2000; 2000WO-US007377. | QY | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| XX | | Db | 61 HPGSHKVPFRKRKHTCPCLNLLCSRPPDGRYRCSMDLNINF 105 |
| PA | (GBTH) GENENTECH INC. | | |
| XX | | | |
| PI | Ashkenazi AJ, Baker KB, Botstein D, Desnoyers L, Eaton DL; | FT | Key |
| PI | Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ; | Peptide | Location/Qualifiers |
| PI | Grimaldi CJ, Gurney AL, Kijavrin IJ, Napier MA, Pan J, Peoni NP; | | 1..19 |
| PI | ROY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, | FT | /note= "B signal sequence" |
| PI | PT Zhang Z, | FT | 20.. 105 |
| XX | | FT | /note= "mature protein" |
| PR | WFP; 2001-03160/04. | FT | Modified-site |
| PR | NP-PSDB; AAF4237. | FT | 33.. 39 |
| DR | | FT | /note= "N-myristoylation site" |
| XX | | FT | 35.. 41 |
| PR | | FT | /note= "N-myristoylation site" |
| XX | | FT | 46.. .52 |
| PR | | FT | /note= "N-myristoylation site" |
| XX | | FT | 88.. 95 |
| PR | | FT | /note= "tyrosine kinase phosphorylation site" |
| XX | | FT | W020075327-A1. |
| PR | | PN | |
| XX | | XX | |
| PR | 14-DEC-2000. | PD | |
| XX | | XX | |
| PR | 24-FEB-2000; 2000WO-US004914. | PR | |
| XX | | XX | |

PR 26-JUL-1999; 99US-0145698P.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Hillan KJ, Napier MA, Watanabe CK, Wood WI;
 XX WPI; 2001-071078/08.
 DR N-PSDB; AAC84469.
 XX
 PT Compositions for inhibiting neoplastic cell growth and treating tumor, a
 cancer, comprises novel PRO186 or PRO184 polypeptides or its agonist.
 XX Claim 31; FIG 2; 104pp; English.
 PS
 XX
 CC The invention provides PRO186 and PRO184 polypeptides that can be used
 for the inhibition of neoplastic cell growth and for treating tumors.
 CC The PRO polypeptides can be expressed by standard recombinant
 methodology. The PRO polypeptides or their agonists are useful for
 inhibition of neoplastic cell growth and for treating tumor, cancers
 such as breast, ovarian, renal, colorectal, uterine, lung,
 bladder or central nervous system cancers or melanoma and leukemia. The
 present sequence represents the human PRO186 polypeptide (encoding cDNA
 Clone ID: DNAG0621-1516)
 CC Sequence 105 AA;
 XX
 SQ

Query Match 100.0%; Score 589; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54; Gaps 0;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGACTCAISWLRGLMCTPLGREGEC 60
 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGACTCAISWLRGLMCTPLGREGEC 60
 QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLNKNINF 105
 Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLNKNINF 105

RESULT 9
 ABA8067
 ID ABA8067 standard; protein; 105 AA.

XX
 AC
 XX
 DT 19-MAR-2001 (first entry)

XX DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
 XX
 KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;
 KW immunosuppressive; cytotoxic; neuroprotective; gastrointestinal;
 KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;
 KW antifebrility; cerebroprotection; nootropic; antidiulcer; antifungal;
 KW anticonvulsant; tranquilizer; neuroleptic; vasotropics; gynecological;
 KW keratolytic; protozoacide; gene therapy.
 XX OS Homo sapiens.
 XX
 PN WO200070049-A2.

XX PD 23-NOV-2000.
 XX
 PF 19-MAY-2000; 2000WO-US013975.
 PR 15-JUL-1999; 99US-0134949P.
 PR 30-JUL-1999; 99US-0144270P.
 PR 04-OCT-1999; 99US-0157508P.
 PA (INCYT) INCYTE GENOMICS INC.
 XX
 PI Tang YT, Rue H, Lai P, Burford N, Bandman O, Baughn MR;

PR Azimzai Y, Lu DAM, Patterson C;
 XX
 DR WPI; 2001-025021/03.
 N-PSDB; AAC84303.
 XX
 PT New human extracellular signaling nucleic acids and polypeptides useful
 for diagnosing, treating and preventing infections and gastrointestinal,
 neurological, reproductive, and autoimmune/inflammatory disorders.
 XX
 PS Claim 1; Page 89; 114pp; English.
 XX
 CC The invention provides human extracellular signaling molecules (EXCS) and
 polynucleotides which identify and encode EXCS. EXCS can be expressed by
 standard recombinant methodology. The amino acid and nucleic acid
 sequences of EXCS are useful for diagnosing, treating and preventing
 infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis),
 neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke),
 reproductive (infertility, ovulatory defects, endometriosis), autoimmune
 (AIDS), Addison's disease), and cell proliferative disorders including
 cancers (of the breast, adrenal gland, bone). They may also be used to
 treat fatal familial insomnia, nutritional and metabolic diseases of the
 nervous system, myopathies, mental disorders (anxiety, schizophrenia,
 mood), as well as infections caused by parasites (malaria, leishmania,
 trypanosoma), viral (adenovirus, coronaviruses, flavivirus), bacterial
 (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus,
 blastomycetes, dermatophytes) agents. The nucleic acids, polypeptides,
 antagonists, agonists, pharmaceutical compositions, and antibodies may
 also be used for treating or preventing disorders associated with
 increased or decreased expression or activity of EXCS. EXCS
 polynucleotides may also be used to detect and quantify gene expression
 in biopsied tissues in which expression of EXCS may be correlated with
 the disease, to determine presence or excess expression of EXCS, to
 monitor regulation of EXCS levels during therapeutic intervention, to
 detect the presence of associated disorders, as targets in microarray, to
 generate hybridization probes, and to detect differences in gene
 sequences among normal, carrier or affected individuals. Antibodies may
 also be used in diagnosing disorders in monitoring patients being
 treated with EXCS agonists, antagonists or inhibitors. Sequences ABA8057
 CC -BA8082 represent the EXCS of the invention
 XX
 SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.8e-54; Gaps 0;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGACTCAISWLRGLMCTPLGREGEC 60
 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGACTCAISWLRGLMCTPLGREGEC 60
 QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLNKNINF 105
 Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLNKNINF 105

RESULT 10
 AAM5073
 ID AAM5073 standard; protein; 105 AA.
 XX
 XX AAM5073;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Endocrine gland-derived vascular endothelial growth factor.
 XX Endocrine gland-derived vascular endothelial growth factor.
 KW Endocrine gland-derived vascular endothelial growth factor; EG-VEGF;
 KW human; cell proliferation; cell migration; fenestration;
 KW cell differentiation; angiogenesis; chemotaxis; endocrine; infertility;
 KW fertility; polycystic ovary syndrome; ovarian cyst; cancer; cytostatic;
 KW diagnosis; therapy.
 XX
 OS Homo sapiens.

| Key | location/Qualifiers |
|-----------|---|
| Peptide | 1..19 |
| | /label= Signal_peptide |
| Protein | 20..105 |
| | /label= Mature_protein |
| FT | |
| FT | Modified-site 33 /note= "N-myristoylated" |
| FT | Modified-site 35 /note= "N-myristoylated" |
| FT | Modified-site 46 /note= "N-myristoylated" |
| FT | |
| FT | W0200200711-A2. |
| XX | |
| XX | 03-JAN-2002. |
| PD | |
| PD | 22-JUN-2001; 2001WO-US020116. |
| PF | |
| PF | 23-JUN-2000; 2000US-0213637P. |
| PR | |
| PR | 07-SEP-2000; 2000US-0200978P. |
| PR | 01-DEC-2000; 2000WO-US0312678. |
| XX | |
| PA | (GETH) GENENTECH INC. |
| XX | |
| PA | Ferrara N, Watanabe C, Wood WI; |
| XX | |
| DR | WPI; 2002-130882/17. |
| XX | |
| PT | New endocrine gland-vascular endothelial growth factor (EG-VEGF) polypeptides, agonists and antagonists, useful for regulating fertility, and for treating cancer of the reproductive organs, e.g. ovarian or prostate cancer. |
| XX | |
| PS | Claim 12; Fig 2; 133pp; English. |
| XX | |
| CC | The present sequence is that of a novel, tissue-restricted, growth and differentiation factor termed endocrine gland-derived vascular endothelial growth factor (EG-VEGF). The sequence is predicted from the open reading frame of a cDNA clone (see ABA91567) obtained from an ovarian tissue library. EG-VEGF induces proliferation, migration and fenestrations in capillary endothelial cells from endocrine glands, but has no effect on a variety of other endothelial and non-endothelial cell types tested. The EG-VEGF precursor has a predicted mol. wt. of 11715 and a pI of 9.05. The mature protein (mol. wt. 8600) is cysteine-rich and is predicted to consist of a series of short beta strands with large connecting loops held together by disulfide bonds resulting in a flat fold with finger-like projections that act as interactive surfaces. 80% homology and 63% identity is shown to venom protein A (VPA) of the black mamba snake, and 76% homology and 58% identity to human protein Bv6. EG-VEGF nucleic acids and polypeptides, as well as agonists and antagonists, can be used in the treatment of conditions associated with hormone-producing tissue, especially ovarian, testicular, cervical, adrenal, placental or prostate tissue. The condition may be polycystic ovary syndrome, cancer, especially ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cyst (all claimed). Fertility can be regulated using an EG-VEGF antagonist to inhibit follicle maturation or ovulation. Methods are claimed for identifying compounds that modulate EG-VEGF activity, especially the ability to induce phosphorylation of a kinase involved in cell proliferation or survival, to induce chemotaxis, angiogenesis, or cell differentiation, or to induce endothelial cell proliferation. |
| CC | Sequence 105 AA; |
| SQ | |
| Query | Match |
| Best | Local Similarity 100.0%; Score 589; DB 5; Length 105; |
| Matches | 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Oy | 1 MRGATRVSMLLTVTSDGAVTGATGACERVQGAGTCATSLWLRGLRMTPLGRGEGEC 60 |
| | 1 MRGATRVSMLLTVTSDGAVTGATGACERDVGAGTCATSLWLRGLRMTPLGRGEGEC 60 |
| Db | |
| Qy | 61 HPGSHKVPFRKRHHTCPCLPNLCSRFPDGRYRCMSDLKINP 105 |
| Db | 61 HPGSHKVPFRKRHHTCPCLPNLCSRFPDGRYRCMSDLKINP 105 |
| RESULT | 11 |
| AAU83674 | |
| ID | AAU83674 standard; protein; 105 AA. |
| XX | |
| AAU83674; | |
| AC | |
| XX | 08-MAY-2002 (first entry) |
| DT | |
| XX | Human PRO protein, seq ID No 166. |
| DE | |
| XX | Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; tumour necrosis factor-alpha. |
| KW | |
| XX | Homo sapiens. |
| OS | |
| XX | |
| PN | W020020288-A2. |
| XX | |
| PD | 31-JAN-2002. |
| XX | |
| PF | 29-JUN-2001; 2001WO-US021065. |
| XX | |
| PR | 20-JUL-2000; 2000US-0219556P. |
| PR | 25-JUL-2000; 2000US-0220605P. |
| PR | 25-JUL-2000; 2000US-0220607P. |
| PR | 25-JUL-2000; 2000US-0220624P. |
| PR | 25-JUL-2000; 2000US-0220638P. |
| PR | 25-JUL-2000; 2000US-0220664P. |
| PR | 25-JUL-2000; 2000US-0220666P. |
| PR | 26-JUL-2000; 2000US-0220893P. |
| PR | 28-JUL-2000; 2000WO-US020710. |
| PR | 01-AUG-2000; 2000US-0222425P. |
| PR | 22-AUG-2000; 2000US-027113P. |
| PR | 23-AUG-2000; 2000WO-US023522. |
| PR | 24-AUG-2000; 2000WO-US023328. |
| PR | 10-NOV-2000; 2000WO-US030873. |
| PR | 28-NOV-2000; 2000US-0233646P. |
| PR | 01-DEC-2000; 2000WO-US032678. |
| PR | 20-DEC-2000; 2000US-00747259. |
| PR | 20-DEC-2000; 2000WO-US034956. |
| PR | 28-FEB-2001; 2001WO-US006520. |
| PR | 01-MAR-2001; 2001WO-US06665. |
| PR | 22-MAR-2001; 2001US-00016744. |
| PR | 10-MAY-2001; 2001US-00054208. |
| PR | 25-MAY-2001; 2001WO-US017092. |
| XX | |
| PA | (GETH) GENENTECH INC. |
| XX | |
| PI | Baker KP, Desnoyers L, Gerritsen ME, Godowski A, Godowski PU; |
| PI | Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI; |
| XX | |
| DR | WPI; 2002-172001/22. |
| DR | N-PSDB; ABK33618. |
| XX | |
| PT | One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors, such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor. |
| PT | |
| PS | Claim 11; Fig 166; 359pp; English. |

CC agonists and antagonists are useful for treating a PRO related disorder.

CC The PRO polypeptides are useful for diagnosing tumours, especially lung.

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or.

CC liver tumour. The PRO polypeptides are useful for stimulating the

CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for

CC stimulating the release of tumour necrosis factor-alpha from human blood,

CC for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular

CC weight markers and for tissue typing. The PRO nucleic acids have

CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO

CC protein sequences of the invention.

XX sequence 105 AA;

SQ

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR

PR 20-DEC-2000; 2000WO-US034956.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-0076769.

PR 22-FEB-2001; 2001US-0079648.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001US-0080666.

PR 09-MAR-2001; 2001US-0080276.

PR 14-MAR-2001; 2001US-0080869.

PR 22-MAR-2001; 2001US-0081674.

PR 05-APR-2001; 2001US-00828166.

PR 10-MAY-2001; 2001US-0085420.

PR 10-MAY-2001; 2001US-0085420.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866028.

PR 23-MAY-2001; 2001WO-US017052.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX

PA (GPTH) GENENTECH INC.

XX

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gueney AL, Hillan KJ, Masters SA, Pan J, Paoni MF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX

DR WPI; 2002-09051612.

DR N-PSDB; ABL88157.

XX

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

XX

PT

XX

AC ABB84902;

XX

DT 16-MAY-2002 (first entry)

XX

DE Human Pro1186 protein sequence SEQ ID NO:172.

XX

KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

KW vulnerability; antiarteriolarclerotic; PRO agonist; pro-agonist; trauma;

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;

KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

KW age-related macular degeneration; arterial restenosis; angina;

KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;

KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

KW wound healing; chromosome mapping; gene mapping.

XX

OS Homo sapiens.

XX

PN WO200200690-A2.

XX

PD 03-JAN-2002.

XX

PF 20-JUN-2001; 2001WO-US019692.

XX

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.8e-54; Mismatches 0; Indels 0; Gaps 0;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR

PR 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000US-02206710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-0043657.

PR 23-AUG-2000; 2000US-0023522.

PR 24-AUG-2000; 2000US-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-0064610.

PR 18-SEP-2000; 2000US-0065350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000US-US0310952.

PR 10-NOV-2000; 2000US-US030873.

PR 01-DEC-2000; 2000WO-US032678.

XX

RESULT 13

AA015527

TD AA015527 standard; protein: 105 AA.

XX

AA015527;

XX

DT 24-OCT-2002 (first entry)

XX

DE Human physiologically-active ZAQ ligand-related protein 3.

XX Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease; colitis; diarrhoea. OS Homo sapiens. XX WO200257443-A1.. XX PD 25-JUL-2002. XX PR 21-JAN-2002; 2002WO-JP000378. XX PR 22-JAN-2001; 2001JP-00013027. XX PR 17-MAY-2001; 2001JP-00147759. XX PA (TAKE) TAKEDA CHEM IND LTD. XX PI Yamada T, Suenaga M, Nishimura O; XX PI WPI; 2002-56801/60. XX DR WPI; 2002-56801/60. XX PT Industrial production of physiologically-active ZAQ ligand by expressing PT in transformant prokaryote and refolding in redox buffer, for use in PT preventing or treating digestive diseases e.g. colitis and diarrhea. XX PR Example 3; Page 76-77; 93pp; Japanese. XX CC The invention comprises a method for producing an active peptide that has CC the same activity as a ZAQ ligand isolated from eukaryotic cell. The CC method of the invention is useful for the production of a physiologically CC -active ZAQ ligand for use in preventing or treating digestive diseases CC (e.g. colitis and diarrhea). The present amino acid sequence represents a CC human physiologically active ZAQ ligand-related protein XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105; Best Local Similarity 100.0%; Pred. No. 3.8e-54; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCGCAISLWLRGLRMCPLGREGEC 60 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCGCAISLWLRGLRMCPLGREGEC 60

QY 61 HPGSHKVPPFRKRKRHTCPCLPNLICSRFPDGGRYRCSDMLKINF 105 Db 61 HPGSHKVPPFRKRKRHTCPCLPNLICSRFPDGGRYRCSDMLKINF 105

RESULT 14 ABB06308 ID ABB06308 standard; protein; 105 AA. XX AC ABB06308; XX DT 27-MAY-2002 (first entry) XX Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23. XX KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide; KW ZAQ; antidiarrheic; laxative; drug development; digestive disease; diarrhoea; KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy. OS Homo sapiens. XX PN WO200205483-A1.. XX PD 24-JAN-2002. XX PR 17-JUL-2001; 2001WO-JP006162. XX PR 18-JUL-2000; 2000JP-0017442. XX PR 02-FEB-2001; 2001JP-00026779. XX PA (TAKE) TAKEDA CHEM IND LTD. XX PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y; XX PI Hinuma S; XX DR N-PSB; ABL49637. XX DR WPI; 2002-188546/24. XX PT Physiologically-active peptides from cows milk, useful for developing PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases PT like colitis, diarrhea, constipation and poor-absorption syndrome, by PT gene therapy. XX PR Claim 5; Page 61; 191pp; Japanese. XX CC The present invention describes a peptide containing an amino acid CC sequence (1) identical to or substantially similar to that of the CC sequences in ABB06305 or ABB06306, or its salt. (1) has anti-diarrheic and CC laxative activities. The peptides and encoding DNA from the present invention are useful for developing drugs to treat digestive diseases CC like colitis, diarrhea, constipation and poor-absorption syndrome, CC including gene therapy. The physiologically-active peptides are applicable as a specific ligand of brain-originated orphan G CC protein-coupled receptor protein ZAQ. ABL49635 to ABB0659 and ABB06303 CC to ABB06315 represent sequence used in the exemplification of the CC present invention. XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105; Best Local Similarity 100.0%; Pred. No. 3.8e-54; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCGCAISLWLRGLRMCPLGREGEC 60 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCGCAISLWLRGLRMCPLGREGEC 60

QY 61 HPGSHKVPPFRKRKRHTCPCLPNLICSRFPDGGRYRCSDMLKINF 105 Db 61 HPGSHKVPPFRKRKRHTCPCLPNLICSRFPDGGRYRCSDMLKINF 105

RESULT 15 AAE24382 ID AAE24382 standard; protein; 105 AA. XX AC AAE24382; XX DT 04-OCT-2002 (first entry) XX DB Human prokineticin 1 precursor protein. XX KW Human; prokineticin 1; gastrointestinal motility; intestinal cancer; KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea; KW diabatic gastroparesis; chronic constipation; malabsorptive disorder; KW inflammatory bowel disorder; analgesic; infection; infectious disease. XX OS Homo sapiens. XX KW Key Location/Qualifiers FT Peptide 1..19 FT /label= signal_peptide FT Protein 20..105 FT /note= "Mature human prokineticin 1" XX PN WO200236625-A2. XX PD 10-MAY-2002. XX PR 01-NOV-2001; 2001WO-US047969. XX PR 03-NOV-2000; 2000US-0245882P. XX PR 03-NOV-2000; 2000US-0245882P.

XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zhou Q, Ehrt FU;
 XX
 DR WPI; 2002-479752/1.
 XX
 DR -PSDB; AAD39321.

XX
 PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
 PT gastrointestinal smooth muscle contraction, useful for improving impaired
 PT gastrointestinal motility in irritable bowel syndrome, chronic
 PT constipation.

XX
 PS Example 1; Fig 1; 86PP; English.

CC The invention relates to human prokineticin 1 and 2 polypeptides that
 CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
 CC molecules encoding such polypeptides. Polypeptides of the invention are
 CC useful for treating disorders involving impaired gastrointestinal
 CC motility. They are useful for stimulating gastrointestinal motility in
 CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
 CC operational ileus, chronic constipation and gastrointestinal reflux
 CC disease. The prokineticin antagonists are useful for inhibiting
 CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
 CC disorders, inflammatory bowel disorders, infectious diseases and
 CC intestinal cancer. The antagonists also act as analgesics. The present
 CC sequence is human prokineticin 1 precursor protein

XX
 SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.8e-54; Matches 105; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSMLLIVVSDCAVITGACERVOGAGTCCALISWLRGLMTPGREGEC 60
 DB 1 MRGATRVSMLLIVVSDCAVITGACERVOGAGTCCALISWLRGLMTPGREGEC 60
 QY 61 HPGSHKVPFRKRAHTCPQLPNLCSRPPDGRYRCMSDLKINP 105
 DB 61 HPGSHKVPFRKRAHTCPQLPNLCSRPPDGRYRCMSDLKINP 105

Search completed: March 30, 2006, 17:30:56
 Job time : 192 secs

1000

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2006, 17:31:17 ; Search time 39 Seconds

(Without alignments) 259.045 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLNVTSDCA.....CSRFPDGRYRCMSMDLQKINP 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

listing first 45 summaries

Database : PIR_80+*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score %

Query Length DB ID

Description

| Result No. | Score | Query | Length | DB ID | Description |
|------------|-------|-------|--------|-----------|---------------------------------------|
| 1 | 100.5 | 17.1 | 350 | 2 JCT188 | REIC protein - human |
| 2 | 88.5 | 15.0 | 640 | 2 T08179 | LRG5 protein - Chl hypothetical prote |
| 3 | 83 | 14.1 | 1101 | 2 T16840 | notch4 - mouse |
| 4 | 81 | 13.8 | 1964 | 1 T09059 | collase precursor |
| 5 | 79 | 13.4 | 112 | 1 XLUH | adhesive plaque pr |
| 6 | 77.5 | 13.2 | 473 | 2 A56175 | cysteine-rich prot |
| 7 | 77 | 13.1 | 251 | 2 A55035 | MEGF6 protein - ra |
| 8 | 75.8 | 12.8 | 1574 | 2 T13954 | ferrillin beta cha |
| 9 | 75 | 12.7 | 734 | 2 JC4861 | notch 3 protein - |
| 10 | 75 | 12.7 | 2318 | 2 S45306 | notch homolog - se |
| 11 | 75 | 12.7 | 2311 | 2 T31070 | collase precursor |
| 12 | 74 | 12.6 | 112 | 2 T151909 | hypothetical prote |
| 13 | 74 | 12.6 | 1620 | 2 T27283 | tumor necrosis fac |
| 14 | 73 | 12.4 | 461 | 1 A35356 | laminin alpha-1 ch |
| 15 | 73 | 12.4 | 3075 | 2 S14458 | hypothetical prote |
| 16 | 72.5 | 12.3 | 643 | 2 T25473 | fibrillin I - bovi |
| 17 | 72.5 | 12.3 | 2871 | 2 A55567 | fibrillin I precursor |
| 18 | 72.5 | 12.3 | 3002 | 2 A47221 | laminin gamma-1 ch |
| 19 | 72 | 12.2 | 1639 | 1 MNFB2 | acroganrin - guine |
| 20 | 71.5 | 12.1 | 148141 | | fibrillin 1 precursor |
| 21 | 71.5 | 12.1 | 601 | 2 B36346 | fibrillin 1 precursor |
| 22 | 71.5 | 12.1 | 683 | 2 C36346 | fibrillin 1 precursor |
| 23 | 71.5 | 12.1 | 178 | 1 A39804 | thrombospondin pre |
| 24 | 71.5 | 12.1 | 1854 | 2 T13576 | hypothetical prote |
| 25 | 71 | 12.1 | 286 | 2 S34665 | collagen, cuticula |
| 26 | 71 | 12.1 | 593 | 1 GYHU | granulin precursor |
| 27 | 70.5 | 12.0 | 1847 | 2 T18308 | probable vitelline |
| 28 | 70.5 | 12.0 | 524 | 2 A55624 | fibrillin-1 precursor |
| 29 | 69.5 | 12.0 | 2871 | 2 A55624 | hypothetical prote |
| 30 | 69.5 | 11.8 | 949 | 2 T24294 | |
| 31 | 69.5 | 11.8 | 2352 | 2 T30201 | heterotrimeric G-prote |
| 32 | 69.5 | 11.8 | 4545 | 1 S25111 | alpha-2-macroglobu |
| 33 | 69 | 11.7 | 2918 | 2 A54105 | fibrillin-2 precursor |
| 34 | 69 | 11.7 | 3133 | 2 S52083 | hemocytin silkwo |
| 35 | 69 | 11.7 | 3712 | 2 S18253 | laminin alpha-1 ch |
| 36 | 68.5 | 11.6 | 728 | 2 T150719 | C-Delta-1 - chick |
| 37 | 68.5 | 11.6 | 850 | 2 T14450 | serine/threonine k |
| 38 | 68.5 | 11.6 | 884 | 2 T18649 | hypothetical prote |
| 39 | 68.5 | 11.6 | 1172 | 2 A42587 | thrombospondin 2 p |
| 40 | 68.5 | 11.6 | 1376 | 2 G00943 | osfemidogen - hum |
| 41 | 68 | 11.5 | 112 | 2 A46717 | collase precursor |
| 42 | 68 | 11.5 | 345 | 2 T25137 | hypothetical prote |
| 43 | 68 | 11.5 | 358 | 2 T25137 | nerve growth facto |
| 44 | 68 | 11.5 | 427 | 1 GQHUN | mannosyl-oligosacc |
| 45 | 68 | 11.5 | 547 | 2 A33901 | |

ALIGNMENTS

RESULT 1

JCT188

REIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C;Accession: JCT188

R;Tougi, T.; Miyazaki, M.; Sakauchi, M.; Inoue, Y.; Namba, M.

Biomed. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-d

A;Reference number: JCT188; MUID:20119095; PMID:10652205

A;Accession: JCT188

A;Molecule type: mRNA

A;Residues: 1-350 <TSU>

A;Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo

C;Genetics:

A;Gene: reic

C;Superfamily: human REIC protein

C;Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match

Best Local Similarity

37.7%; Pred. No.

0.0086; DB

2; length

350; Matches

26; Conservative

3; Mismatches

29; Indels

11; Gaps

4; Query

26 CERVOQGAGTCCLISIMLWRLGI--RMCTPLGRGSRGCRCH-PGSHKVPRKRKH----HT

Db

208 CNDRDCQGQCCAFQ--RGLLPPVCTPLPVGBLCHDPASRLIDLTWELBDGALDR

264

RESULT 2

T08179

LRG5 protein - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T08179

R;Gloeckner, G.; Beck, C.F.

A;47221

submitted to the EMBL Data Library, October 1996

A;Description: Molecular characterization of a gene (LRG5) involved in blue light signal

A;Reference number: Z16399

A;Accession: T08179

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-640 <GL>

A;Cross-references: UNIPROT:Q96397; UNIPARC:UPI000009E362; EMBL:U73817; NID:91644369; PI

C;Genetics:

A;Gene: LRG5

Query Match 15.0%; Score 88.5; DB 2; Length 640;
 Best Local Similarity 31.6%; Pred. No. 0.23; Mismatches 5; Indels 23; Gaps 4;
 Matches 24; Conservative 5; MisMatches 24; Indels 23; Gaps 4;

Qy 32 CGACTTCAISLWLRGLRMCTPLSRGEGCHPSHVKVPPRKHHTCPCLPNLCSRF-- 89
 Db 488 CTAGRCC----WM---TCLPMMGSGGTWPWRPLMTP----SRTCACTLPCCSRWLR 533

Qy 90 ----PDGRYRCSM 98
 Db 534 RWRGGWAPGGRWRCSL 549

RESULT 3

T16840 hypothetical protein T10B10.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T16840
 C;Submitted to the EMBL Data Library, October 1995

A;Description: The sequence of *C. elegans* cosmid T10B10.

A;Reference number: Z18588

A;Accession: T16840

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1101 <GET>

A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:91049339; PI: C;Genetics:

A;Experimental source: strain Bristol N2

A;Gene: CESP:T10B10.4

A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 14.1%; Score 83; DB 2; Length 1101;
 Best Local Similarity 24.4%; Pred. No. 1.3%;
 Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;

Qy 13 LVTVNSDCAVITGACERDVQCGAGTCATSLWLRG----- 46
 Db 749 LMSVQRCAMGIGCPPGNOCENGVCCPMPMCSSSIASSVCGMANSCPFIGYCEGRGCL 807

Qy 47 -LWNTPLGR-----SCEEECHG-----SHVPPFRKRKHTCPCLPNLCS 87
 Db 808 EPLPLCPNPGGRASMSCYRGAECPGAGCTPLGGCCLLSMEPVCPTRSNAVCQSPNNVC- 866

Qy 88 RFPDGRYRCSM 98
 Db 867 -PSGA-SCTM 874

RESULT 4

T09059 notch4 - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09059
 R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
 submitted to the EMBL Data Library, October 1997

A;Description: Sequence of the mouse major histocompatibility locus class III region.

A;Reference number: Z16543

A;Accession: T09059

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1964 <ROW>

A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7FL; EMBL:AF030001; NID:92564945; C;Genetics:

A;Gene: notch4

A;Map position: 17
 A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67

A;Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C;Keywords: receptor; signal transduction
 P;P14-545/Domain: EGF homology <EGF>

Query Match 13.4%; Score 79; DB 1; Length 112;
 Best Local Similarity 28.4%; Pred. No. 0.48; Mismatches 45; Indels 24; Gaps 6;
 Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;

Qy 9 IMMLVNTSDCAVITG-----ACERDVQCGAGTCATSLWLRGLRMCTPLSRG 56
 Db 5 LILLIVAVSVAYAPGRRGIGITINLENGELCNSAQC-KSNCCOHSSAL-GLARCTSWAE 62

Qy 57 GECBPGSHVKVPPRKHHTCPCLPNLCSRFPPDGRYRCSMDLKNITP 105

| | | |
|--|---|--|
| Db | 63 NSBC--SVKTLV--GIVYKCPGERGLTC--EGDKTIVGSITNTNF 101 | Genomics 51, 27-34, 1998 |
| A;Title: | Identification of high-molecular-weight proteins with multiple EGF-like motifs in | A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs in |
| A;Reference number: | Z14126; MUID:98360089; PMID:9693030 | A;Reference number: Z14126; MUID:98360089; PMID:9693030 |
| RESULT 6 | | |
| A5175 | adhesive plaque protein MgfP2 precursor - Mediterranean mussel | A;Accession: T1354 |
| C;Species: | Mytilus galloprovincialis (Mediterranean mussel) | A;Status: preliminary; translated from GB/EMBL/DBJ |
| C;Date: | 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004 | A;Molecule type: mRNA |
| C;Accession: | A5175 | A;Residues: 1-1574 <Ntk> |
| R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S. | A;Cross-references: UNIPROT:025464; UNIPARC:UPI00012aB7B; GB:D43794; NID:9602767; PIDN: F1-117; Domain: signal sequence #status predicted <SIG> | A;Cross-references: UNIPROT:088281; UNIPARC:UPI000043BBB; EMBL:AB011532; NID:93449293; E |
| J. Biol. Chem. 270, 6588-6701, 1995 | A;Cross-references: UNIPROT:025464; UNIPARC:UPI00012aB7B; GB:D43794; NID:9602767; PIDN: F,387-419; Domain: EGF homology <EGF> | A;Experimental source: strain Sprague-Dawley; brain |
| F,429-460; Domain: EGF homology <EGF> | A;Genetics: | |
| F,36,43,56,57,382,424,455,486,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) # | A;Gene: MEGF6 | |
| Query Match 13.2%; Score 77.5; DB 2; Length 473; | Query Match 12.8%; Score 75.5; DB 2; Length 1574; | |
| Best Local Similarity 31.2%; Pred. No. 2,3; | Best Local Similarity 28.6%; Pred. No. 10; | |
| Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7; | Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4; | |
| Qy 26 CERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCH-POSSHKVFFRKRKHRTC--PCL 81 | Qy 19 CAVITGAC---ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHKVKPPRKR 73 | |
| Db 117 QEKV-CSPNPK-----RNKGKCSPLGKGYKTCGCGGTYG--RCEVACKPNPK 165 | Db 755 CHRVYGBCPCKPGKRTGEBGAD--CPBCRWGLGCQBCPACENGASCP----- 801 | |
| Qy 82 PNLICSRFPDR-YRC 96 | Qy 74 KHNTPCPNLUCSRFPDGRYRC 97 | |
| Db 166 NKGRC--FPDKGTGKYC 180 | Db 802 ETGCLCLCPGPVSSRCQD--TGS 822 | |
| RESULT 7 | | |
| A5035 | cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi) | |
| C;Species: | Enchytraeus buchholzi | |
| C;Date: | 14-Nov-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 | |
| C;Accession: | A5035; S45034 | |
| R;Willum, J.; Schmitz-Wrede, H.P.; Greven, H.; Wunderlich, F. | C;Keywords: glycoprotein; integrin alpha, disintegrin homology | |
| J. Biol. Chem. 269, 24688-24691, 1994 | C;Accession: JC4861 | |
| A;Title: cDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-mi | R;Gupta, S.K.; Alves, K.; O'Neil Palladino, I.; Mark, G.E.; Hollis, G.F. | |
| A;Reference number: A55035; MUID:95014230; PMID:7929141 | Biochem. Biophys. Res. Commun. 224, 318-22, 1996 | |
| A;Accession: A55035 | A;Title: Molecular cloning of the human fertilin beta subunit. | |
| A;status: preliminary | A;Reference number: JC4861; MUID:96295488; PMID:8702389 | |
| A;Molecule type: mRNA | A;Accession: JC4861 | |
| A;Residues: 1-251 <WIL> | A;Molecule type: mRNA | |
| A;Cross-references: UNIPROT:Q24774; UNIPARC:UPI00007D243; EMBL:X79344; NID:9488802; PID | A;Residue: 1-734 <WUP> | |
| C;Superfamily: ultra-high-sulfur keratin | A;Cross-references: UNIPROT:Q9965; UNIPARC:UPI000161BD9; GB:U38805; NID:94151118; PIDN | |
| Query Match 13.1%; Score 77; DB 2; Length 251; | C;Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in | |
| Best Local Similarity 30.9%; Pred. No. 1,5; | C;Superfamily: mouse meltrin alpha, disintegrin homology | |
| Matches 25; Conservative 7; Mismatches 45; Indels 4; Gaps 3; | C;Keywords: glycoprotein; integrin alpha, disintegrin homology | |
| Qy 17 SDCAVITGACERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHKVKPPRKRHH 76 | F,382-734/Protein: fertilin beta chain #status predicted <NAT> | |
| Db 77 SQCKCERGCKKG--CKEG-CGCAKPGKVAGCCGCGCKCCKGECKPGCTKRCCTKCGVE 133 | F,388-467; Domain: disintegrin homology <DIS> | |
| Qy 77 TPCCLPNLUCSRFPDRYRC 97 | F,448-450; Region: integrin binding #status predicted | |
| Db 134 DCPCGCPCKCKE-GDCKVNC 153 | F,586-708; Domain: transmembrane #status predicted <TM> | |
| RESULT 8 | | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
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| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Qy 15 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | Qy 401 TPSDCAVITGAC-----ERDVQGAGTCCAISLWLRLGRMCTPLGRGEBCHPGSHK 66 | |
| Db 67 VPFFRKRTHTCP 79 | Db 453 LPVCGNGSSASC 465 | |
| Db 453 LPVCGNGSSASC 465 | RESULT 10 | |
| S43306 | Query Match 12.7%; Score 75; DB 2; Length 734; | |
| C;Species: | Best Local Similarity 28.8%; Pred. No. 6; | |
| C;Accession: | Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3; | |
| Q | | |

A: Molecule type: mRNA
 A: Residues: 1-2318 <LAR>
 A: Cross-references: UNIPROT:Q61982; UNIPARC:UPI00002930C; EMBL:X74760; NID:9483580; PID:
 C: Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F: 163-195/Domain: EGF homology <EGF1>
 F: 474-505/Domain: EGF homology <EGF2>
 F: 854-885/Domain: EGF homology <EGF2>
 F: 1839-1871/Domain: ankyrin repeat homology <AN1>
 F: 1902-1941/Domain: ankyrin repeat homology <AN2>
 F: 1906-1938/Domain: ankyrin repeat homology <AN3>
 F: 1939-1971/Domain: ankyrin repeat homology <AN4>
 F: 1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 75; DB 2; Length 2318;
 Best Local Similarity 28.1%; Pred. No. 16; Mismatches 25; Indels 34; Gaps 5;
 Matches 25; Conservative 5; Mismatches 25; Indels 34; Gaps 5;

Qy 19 CAVITGACERDVQGAGTCALISLWLRGLRMCTPLGRGESEC----- 60
 Db 1287 CERVARSC-RELQCPVGPQCQT-ARGSPRACBPGLSGPSCRVSRASPAGTNAASCASA 1343

Qy 61 --HPGS----HKVPPFRGRKHKHTCPCLP 82
 Db 1344 PCHRGGSCLPVSQVPPFR----CVCAP 1366

RESULT 11

T31070 notch homolog - sea urchin (*Lytechinus variegatus*)
 C:Species: *Lytechinus variegatus* (variegated urchin)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T31070
 R:Sherwood, D.R.; McClay, D.R.
 development, 124, 3363-3374, 1997
 A:Title: Identification and localization of a sea urchin Notch homologue: insights into
 A:Reference number: Z20966; MUID:97454256; PMID:931031
 A:Accession: T31070
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1231 <SHE>
 A:Cross-references: UNIPARC:UPI000007B31C; EMBL:AF000634; NID:92570350; PID:92570351; PI
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.7%; Score 75; DB 2; Length 2531;
 Best Local Similarity 29.9%; Pred. No. 17; Mismatches 23; Indels 32; Gaps 5;
 Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

Qy 22 ITGACERDVQGAGTCAL--SLWLRLGRMCTPLGRGESECCHGSGSHKVKPPFRGRKHKHTCP 79
 Db 120 VDNVCKLSPCQNGCCTRLTSLWMDYEC-FCTP-ANTGENCTDDNHCV-----SNP 168

Qy 80 CILPULLCRRFPDSYRC 96
 Db 169 CILNGAVCTSSSDG-YSC 184

RESULT 12

151909 colipase precursor - rat
 N:Alternative names: procolipase
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Accession: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R: Payne, R.M.; Sims, H.F.; Jennings, M.L.; Lowe, M.B.
 Am. J. Physiol. 266, G914-G921, 1994
 A:Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
 A:Reference number: 151909; MUID:94262798; PMID:8203536
 A:Accession: 151909
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-112 <PAY>
 A:Cross-references: UNIPROT:PI17084; UNIPARC:UPI0000127E7C; GB:M58370; NID:9203504; PID:
 \R,Wicker, C.; Puigserver, A.

Biochem. Biophys. Res. Commun. 167, 130-136, 1990
 A:Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition
 A:Reference number: A34623; MUID:90179738; PMID:2129524
 A:Accession: A34623
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-17; V, 19-112 <WTC>
 A:Cross-references: UNIPARC:UPI0000170885; GB:M33333; NID:9203502; PID:AAA40943.1; PID:
 C:Superfamily: colipase
 C:Keywords: lipid digestion; lipid hydrolysis; pancreas
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-112/Product: colipase #status predicted <MAT>
 Query Match 12.6%; Score 74; DB 2; Length 112;
 Best Local Similarity 25.8%; Pred. No. 1.5; Mismatches 24; Indels 20; Gaps 4;
 Matches 24; Conservative 10; Mismatches 39; Indels 20; Gaps 5;

Qy 6 RUSIMILVLTIVSACAVITG-----ACERDVQGAGTCALISLWLRGLRMCTPL 53
 Db 2 KVVLVVLVLTIVAYAARGPRLFINLDEGEICVNMSMC-KSRCCOHTIL-GIARCTH 59

Qy 54 GRGBECKPGSHKVKPPFRGRKHKHTCP1LPNLLC 86
 Db 60 AMENSESSEPKTIVGIVR-----CPRERGLC 86

RESULT 13

T27283 hypothetical protein Y64G10A.f - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27283
 R:Ainscough, R.
 Submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20336
 A:Accession: T27283
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1620 <WTL>
 A:Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;
 A:Experimental source: clone Y64G10A
 C:Genetics:
 A:Gene: CESP:Y64G10A.f
 A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71
 Query Match 12.6%; Score 74; DB 2; Length 1620;
 Best Local Similarity 27.5%; Pred. No. 15; Mismatches 22; Conservative 4; Indels 16; Gaps 4;
 Matches 22; Conservative 4; Mismatches 16; Indels 38; Gaps 4;

Qy 16 VSDCAVITGACERDVQGAG-----TCCATSLWLRGLRMCTPLGRGESECCHGSGSHKVKP 68
 Db 1114 VARCDHVGEC---RCPPAGWTGPDCOTSC-----PLGRGESEC----- 1148

Qy 69 FERKRHKHTCPCLPNULCSR 88
 Db 1149 -----RHSCQCSNGASCDR 1162

RESULT 14

A35356 tumor necrosis factor receptor 2 precursor [validated] - human
 N:Alternative names: 75K tumor necrosis factor receptor; TNF receptor type 2
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A35356; R36475; R484116; A36007; R23667; B55010; I38094
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerry, R.; Dower, S.K.
 Science 248, 1019-1023, 1990
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A:Reference number: A35356; MUID:90260639; PMID:2160731
 A:Accession: A35356
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SM1>

F111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F1160-1361/Domain: IVA <DOMA>
 F1362-1553/Domain: IIA <DOM3A>
 F1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F1452-1506/Domain: laminin-type EGF-like homology <LE18>
 F1509-1553/Domain: laminin-type EGF-like homology <LE19>
 F1554-2125/Domain: I/I, heptad repeats <DOM2>
 F2116-2120/Region: cell adhesion #status predicted
 F2126-3075/Domain: G <DOMG>
 F2142-2300/Domain: laminin G repeat homology <LG1>
 F2329-2484/Domain: laminin G repeat homology <LG2>
 F2510-2676/Domain: laminin G repeat homology <LG3>
 F2531-2536/Region: cell attachment (R-G-D) motif
 F2739-2886/Domain: laminin G repeat homology <LG4>
 F2916-3073/Domain: laminin G repeat homology <LG5>
 F38,164,555,763,801,838,925,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
 rate (Asn) (covalent) #status predicted
 F297-305/bisulfide bonds: #status predicted

Query Match 12.4%; Score 73; DB 2; Length 3075;
 Best Local Similarity 23.0%; Pred. No. 32;
 Matches 23; Conservative 10; Mismatches 35; Indels 32; Gaps 4;
 Qy 19 CAVITGACERBRDVGAGTCAISLWLGRMRMCTPL---GRIGGEECH-----P 62
 Db 1056 CDVVTGHCOCKSKFGGRADQCSILGYDRPDPVCPDCDIRGTSQDAGCNLBEQGLGGCVBT 1115
 Qy 63 GSHKVPFRKRKHTCPCLPNL--CRFPPDARYRCMD 99
 Db 1116 GA-----CPCKENVRGPQCNBCREGTPALRAD 1142

Search completed: March 30, 2006, 17:35:36
 Job time : 41 secs

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OM protein - protein search, using sw model

Run on: March 30, 2006, 17:28:12 ; Search time 230 Seconds
(without alignments)

32.089 Million cell updates/sec
Title: US-10-692-299-2
Perfect score: 589

Sequence: 1 MRGATRVSIMLNLTVSDCA. CSRFPDGRRYRCMSMLKINP 105

Scoring table: BLOSUM62
Gpop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query #
Score Match Length DB ID Description

DESCRIPTION

RESULT 1
PROKL_HUMAN
ID PROKL_HUMAN
STANDARD;
PRT; 105 AA.
AC P51294;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prokinecin 1 precursor (Endocrine-gland-derived vascular growth factor) (EG-VEGF) (Mammal);
GN Name=PROKL; ORFNames=INQ0600/PROL186;
OS Homo Sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoptoglires; Primates; Catarrhini; Hominidae; Homo; OX NCBI_TaxID=9606;
RN [1];
RP NUCLOBONIDE SEQUENCE.
RX MEDLINE:21160229; PubMed:11259612;
RA Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.-Y.;
RT "Identification of two prokinecin cDNAs: recombinant proteins potentially contract gastrointestinal smooth muscle.";
RT Mol. Pharmacol. 59:692-698 (2001).
RN [2];
RP NUCLOBONIDE SEQUENCE.
RX MEDLINE:21419730; PubMed:11528470; DOI=10.1038/35091000;
RA LeGouette J., Kowalski J., Foster J., Hass P., Zhang Z.,
RA Billard-Telm L., Prant G., Rangell L., DeGuzman L., Keller G.-A.,
RA Peale F., Gurney A., Hillan K.J., Ferrara N.;
RT "Identification of an angiogenic mitogen selective for endocrine gland endothelium";
RN Nature 412:877-884 (2001).
RN [3];
RP NUCLOBONIDE SEQUENCE.
RA Fraser C.;
RT "Mambatine, a snake venom related endocrine hormone that controls macrophages";
RT Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases.
RN [4];
RP NUCLOBONIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE:22887296; PubMed:11975109; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.J., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Clark H.F., Gurney A.J., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Guo Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.-H., Robbie E., Sanchez C., Schenfeld J.,
RA Sehagir S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiegand D., Woods K., Xie M.-H., Goddard A.D.,
RA Yansura D.G., Yi S., Yu J., Yuan J., Zhang M., Zhang Z.,
RA Wood W.I., Godowski P.J., Gray A.M.,
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment";
RT Genome Res. 13:2265-2270 (2003).
RN [5];

32 193 32.8 39 2 050861_9MURI
33 126.5 21.5 124 2 056810_PPNMO
34 112 19.0 056811_PCNMO
35 109 18.5 2 056811_PCLC
36 108.5 18.4 221 1 DKK4_MOUSE
37 107.5 18.3 224 1 DKK3_CHICK
38 107.5 18.3 350 1 Q9D34_XENLA
39 104 17.7 255 2 Q4KOF1_TIGTING
40 102 17.3 180 2 DKK2_HUMAN
41 102 17.3 259 1 Q5BHU5_GRCJA
42 101.5 17.2 256 2 Q5BHU6_MOUSE
43 101 17.1 259 1 DKK1_MOUSE
44 101 17.1 272 1 Q8BFW0_mus_muscu
45 101 17.1 272 1 Q8BFW0_mus_muscu
054908 mus muscu

ALIGNMENTS

32 193 32.8 39 2 050861_9MURI
33 126.5 21.5 124 2 056810_PPNMO
34 112 19.0 056811_PCNMO
35 109 18.5 2 056811_PCLC
36 108.5 18.4 221 1 DKK4_MOUSE
37 107.5 18.3 224 1 DKK3_CHICK
38 107.5 18.3 350 1 Q9D34_XENLA
39 104 17.7 255 2 Q4KOF1_TIGTING
40 102 17.3 180 2 DKK2_HUMAN
41 102 17.3 259 1 Q5BHU5_GRCJA
42 101.5 17.2 256 2 Q5BHU6_MOUSE
43 101 17.1 259 1 DKK1_MOUSE
44 101 17.1 272 1 Q8BFW0_mus_muscu
45 101 17.1 272 1 Q8BFW0_mus_muscu
054908 mus muscu

| | | | |
|---------------------------|---|---|--|
| GN | ORFNames=GSTENG0002819001; | SQ | SEQUENCE 108 AA: 11672 MW; C00410399A9B215E CRC64; |
| OS | Tetraodon nigroviridis (Green puffer). | Query Match | 54.0%; Score 318; DB 2; Length 108; |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | Best Local Similarity | 51.9%; Pred. No. 2e-25; |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; | Matches | 54; Conservative 15; Mismatches 27; Indels 8; Gaps 1; |
| OC | Tetradontiformes; Tetradontidae; Tetraodontidae; Tetraodon. | Match | 54; |
| OX | NCBI_TAXID=99883; | 1 | MRCATRIVSMLIV-----TVSDCAVITGACERDVQCGAGTCCASLWIRGLRNCITP 52 |
| RN | NUCLEOTIDE SEQUENCE. | 1 | MRSRCARLLLUUUPPLITPPAGDANVIGACDRQQCGGMCACAVSLWTKSIRCTP 60 |
| RA | Jailon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., | QY | 53 LSRGEGBCHPGSHKVKPFERKRKHTCPCLPNLCSRFPGYRC 96 |
| RA | Maucler E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A., | 61 MGKVGDSHPMTRKVPPFGRMHTCPCLPGLACSRISFPNRYTC 104 | |
| RA | Nicaud S., Jaffe D., Fisher S., Lutfallal G., Desat C., Seguins B., | DB | |
| RA | Basilia C., Salamouba M., Devy M., Boudet N., Castellano S., | | |
| RA | Anthoudou V., Jubin C., Castelli V., Katiika M., Vacherie B., | | |
| RA | Blemon C., Skalli Z., Cattolico L., Poulin J., De Berardinis V., | | |
| RA | Cruaud C., Duprat S., Brottier P., Contanceau J.P., Gouzy J., De Berardinis V., | | |
| RA | Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S., | | |
| RA | Kells M., Volf J.N., Guigo R., Zody M.C., Mestrov J., | | |
| RA | Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., | | |
| RA | Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., | | |
| RA | Wancker P., Lander E.S., Weissenbach J., Roest Crollius H., | | |
| RT | Genome duplication in the teleost fish Tetraodon nigroviridis reveals | | |
| RT | the early vertebrate proto-karyotype.", | | |
| RL | Nature 431:945-957(2004). | | |
| RN | [2] | | |
| RP | NUCLEOTIDE SEQUENCE. | RESULT 8 | |
| RG | Genoscope; Whitehead Institute Centre for Genome Research; | ID | VPRA_DENPO |
| RL | Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. | ID | VPRA_DANPO |
| CC | - - CAUTION: The sequence shown here is derived from an | STANDARD; | |
| CC | preliminary data. | PRT; | 81 AA. |
| CC | EMBL; CAE01014991; CAG07489.1; -; Genomic_DNA. | AC | P25687; |
| FT | NON_TER | DT | 01-MAY-1992 (Rel. 22, Created) |
| FT | SEQUENCE 106 AA; 12098 MW; 8D4DC1B388B3052 CRC64; | DT | 13-SEP-2005 (Rel. 48, Last sequence update) |
| Db | 64 SHKUPPFERKHKHTCPCLPNLCSRFPDRGTYRSMQLKIN 104 | DT | 13-SEP-2005 (Rel. 48, Last annotation update) |
| Db | 65 SHKUPYPGKQHQHTCPCLPFLHMCIRFEDSKYRCIDDFKVD 105 | DE | Intestinal toxin 1 (Mamba intestinal toxin 1) (MIT 1) (MIT1) (Venom protein A). |
| RN | RESULT 7 | DE | Dendroaspis polylepis polylepis (Black mamba). |
| 0863H4 BOVIN | ID | OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; |
| 0863H4 BOVIN PRELIMINARY; | ID | OC | Lepidomorpha; Squamata; Scelopoglossa; Serpentes; Colubroidea; |
| PRT; | ID | OC | Elapidae; Elapine; Dendroaspis. |
| AC | Q863H4 | OX | NCBI_TAXID=8620; |
| AC | Q863H4_ | RN | PROTEIN SEQUENCE OF 1-80. |
| DT | 01-JUN-2003 (TREMBREL 24, Created) | RP | TISSUE_Venom; |
| DT | 01-JUN-2003 (TREMBREL 24, Last sequence update) | RC | TISSUE_Venom, AND CHARACTERIZATION. |
| DT | 01-MAR-2004 (TREMBREL 26, Last annotation update) | RC | PROTEIN SEQUENCE, AND CHARACTERIZATION. |
| DT | 01-MAR-2004 (TREMBREL 26, Last annotation update) | RC | MEDLINE=20036442; PubMed=10161016/S0014-5793(99)01459-3; |
| DE | BBF/prokineticin 2-like protein splice variant. | RC | MEDLINE=20036442; PubMed=10161016/S0014-5793(99)01459-3; |
| OS | Bos taurus (Bovine). | RA | RA Schweiz H., Pacaud P., Diocleti S., Moinier D., Lazdunski M.; |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | RA | "MRTL", a black mamba toxin with a new and highly potent activity on |
| OC | Mammalia; Eutheria; Laurasiatheria; Gextartiodactyla; Ruminantia; | RT | intestinal contraction."; |
| OC | Perovidae; Bovidae; Bovinae; Bos. | RT | FEBS Lett. 461:183-188(1998). |
| OX | NCBI_TaxID=9913; | RT | [3] |
| RN | [1] | RP | STRUCTURE BY NMR OF 1-81, AND DISULFIDE BONDS. |
| RP | NUCLEOTIDE SEQUENCE. | RC | TISSUE_Venom; |
| RP | NUCLEOTIDE SEQUENCE. | RC | MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057; |
| RC | TISSUE-Testis; | RC | Boisbouvier J., Albrant J.-P., Blackledge M., Jaquinod M., |
| RC | TISSUE-Testis; | RC | Schweiz H., Laxdunki M., Marion D., |
| RC | TISSUE-Testis; | RC | "A structural homologue of coilase in black mamba venom revealed by |
| RC | TISSUE-Testis; | RC | NMR floating disulphide bridge analysis.", |
| RC | TISSUE-Testis; | RC | J. Mol. Biol. 283:205-219(1998). |
| CC | "The AVIT protein family.", | CC | - - FUNCTION: Potently contracts gastrointestinal (GI) smooth muscle. |
| CC | "The AVIT protein family.", | CC | May act on potassium channels, but not on Kv1.1, Kv1.2, Kv1.3, Kv1.4, Kv1.5, Kv2.1, Kv3.4, Kv4.2, TRK-1, HERG, KCNQ1, KCNQ2, KCNQ3, IRK1, IRK2, ROMK1, GIRK1, 2 and GIRK1,4. |
| CC | "The AVIT protein family.", | CC | - - SUBCELLULAR LOCALIZATION: Secreated. |
| CC | "The AVIT protein family.", | CC | - - SIMILARITY: Belongs to the prokineticin family. |
| CC | "The AVIT protein family.", | CC | This Swiss-Prot entry is copyright. It is produced through a collaboration |
| CC | "The AVIT protein family.", | CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| CC | "The AVIT protein family.", | CC | the European Bioinformatics Institute. There are no restrictions on its |
| CC | "The AVIT protein family.", | CC | use as long as its content is in no way modified and this statement is not |
| CC | "The AVIT protein family.", | CC | removed. |
| CC | "The AVIT protein family.", | CC | |
| DR | EMBO Rep. 4:4469-473(2003); | DR | PDB; 1INT; NMR; @=1-81. |
| DR | EMBL; AY19258; AAP31907.1; -; mRNA. | KW | 3D-structure; Direct protein sequencing; Toxin. |
| DR | HSSP; P25687; 1INT. | FT | DISULFID; 7 19 |
| DR | INTERPRO; IPR009523; Prokineticin; 1. | FT | DISULFID; 13 31 |
| DR | PANTHER; PTHR18821; Prokineticin; 1. | FT | DISULFID; 18 59 |
| DR | PFAM; PP06607; Prokineticin; 1. | FT | DISULFID; 41 67 |

RT Unstriped Nile Grass Rat (Arvicathis niloticus).";
 RL J. Biol. Rhythms 20:206-218(2005).
 DR EMBL; AY771383.1; -; mRNA.
 SQ SEQUENCE 107 AA; 11597 MW; CFAE8947354361BB CRC64;

Query Match 50.6%; Score 298; DB 2; Length 107;
 Best Local Similarity 49.0%; Pred. No. 2.4e-23; Mismatches 50; Conservative 19; Indels 8; Gaps 1;
 Matches 25; Mismatches 25; DR GO; GO:0005576; C-extracellular region; ISS.
 DR GO; GO:0001664; P-G-protein-coupled receptor binding; ISS.
 DR GO; GO:0000187; P-activation of MAPK; ISS.
 DR GO; GO:0001525; P-angiogenesis; ISS.
 DR GO; GO:0006916; P-anti-apoptosis; ISS.
 DR GO; GO:0008233; P-cell proliferation; ISS.
 DR GO; GO:0006935; P-chemotaxis; ISS.
 DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; ISS.
 DR GO; GO:0006554; P-inflammation response; ISS.
 DR GO; GO:0019233; P-perception of pain; ISS.
 DR GO; GO:0007204; P-positive regulation of cytosolic calcium io. . .; ISS.
 DR GO; GO:0045935; P-positive regulation of smooth muscle contra. . .; ISS.
 DR GO; GO:0007233; P-spermatogenesis; ISS.
 DR Interpro; IPR018821; Prokinecin; 1.
 DR PANTHER; PTHR18821; Prokinecin; 1.
 DR Pfam; PF06607; Prokinecin; 1.
 SQ SEQUENCE 128 AA; 14290 MW; C22CDBDBB40483EC CRC64;

Query Match 50.6%; Score 298; DB 2; Length 128;
 Best Local Similarity 43.5%; Pred. No. 2.4e-23; Mismatches 54; Conservative 15; Indels 28; Gaps 2;
 Matches 54; Mismatches 28; DR GO; GO:0001871; P-G-protein-coupled receptor binding; ISS.
 DR GO; GO:0000187; P-activation of MAPK; ISS.
 DR GO; GO:0001525; P-angiogenesis; ISS.
 DR GO; GO:0006916; P-anti-apoptosis; ISS.
 DR GO; GO:0008233; P-cell proliferation; ISS.
 DR GO; GO:0006935; P-chemotaxis; ISS.
 DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; ISS.
 DR GO; GO:0006554; P-inflammation response; ISS.
 DR GO; GO:0019233; P-perception of pain; ISS.
 DR GO; GO:0007204; P-positive regulation of cytosolic calcium io. . .; ISS.
 DR GO; GO:0045935; P-positive regulation of smooth muscle contra. . .; ISS.
 DR Interpro; IPR018821; Prokinecin; 1.
 DR PANTHER; PTHR18821; Prokinecin; 1.
 DR Pfam; PF06607; Prokinecin; 1.
 SQ SEQUENCE 128 AA; 14290 MW; C22CDBDBB40483EC CRC64;

Query Match 50.6%; Score 298; DB 2; Length 107;
 Best Local Similarity 54.0%; Pred. No. 2.4e-23; Mismatches 47; Conservative 16; Indels 24; Gaps 0; Gaps 0;
 Matches 47; Mismatches 24; DR GO; GO:0001871; P-G-protein-coupled receptor binding; ISS.
 DR GO; GO:0000187; P-activation of MAPK; ISS.
 DR GO; GO:0001525; P-angiogenesis; ISS.
 DR GO; GO:0006916; P-anti-apoptosis; ISS.
 DR GO; GO:0008233; P-cell proliferation; ISS.
 DR GO; GO:0006935; P-chemotaxis; ISS.
 DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; ISS.
 DR GO; GO:0006554; P-inflammation response; ISS.
 DR GO; GO:0019233; P-perception of pain; ISS.
 DR GO; GO:0007204; P-positive regulation of cytosolic calcium io. . .; ISS.
 DR GO; GO:0045935; P-positive regulation of smooth muscle contra. . .; ISS.
 DR Interpro; IPR018821; Prokinecin; 1.
 DR PANTHER; PTHR18821; Prokinecin; 1.
 DR Pfam; PF06607; Prokinecin; 1.
 SQ SEQUENCE 107 AA; 11581 MW; DBDBBA472B5C8045 CRC64;

Query Match 50.6%; Score 298; DB 2; Length 107;
 Best Local Similarity 54.0%; Pred. No. 2.4e-23; Mismatches 47; Conservative 16; Indels 24; Gaps 0; Gaps 0;
 Matches 47; Mismatches 24; DR GO; GO:0001871; P-G-protein-coupled receptor binding; ISS.
 DR GO; GO:0000187; P-activation of MAPK; ISS.
 DR GO; GO:0001525; P-angiogenesis; ISS.
 DR GO; GO:0006916; P-anti-apoptosis; ISS.
 DR GO; GO:0008233; P-cell proliferation; ISS.
 DR GO; GO:0006935; P-chemotaxis; ISS.
 DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; ISS.
 DR GO; GO:0006554; P-inflammation response; ISS.
 DR GO; GO:0019233; P-perception of pain; ISS.
 DR GO; GO:0007204; P-positive regulation of cytosolic calcium io. . .; ISS.
 DR GO; GO:0045935; P-positive regulation of smooth muscle contra. . .; ISS.
 DR Interpro; IPR018821; Prokinecin; 1.
 DR PANTHER; PTHR18821; Prokinecin; 1.
 DR Pfam; PF06607; Prokinecin; 1.
 SQ SEQUENCE 107 AA; 11581 MW; DBDBBA472B5C8045 CRC64;

RESULT 15
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 ID Q863H5_BOVIN PRELIMINARY; PRT; 128 AA.
 AC Q863H5;
 DT 01-JUN-2003 (Tremblie. 24, Created)
 DT 01-JUN-2003 (Tremblie. 24, Last sequence update)
 DR 01-MAR-2004 (Tremblie. 26, Last annotation update)
 DR Prokinecin 2-like protein.
 OS Bos taurus (Bovine).
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Testis;
 RX MEDLINE-22612805; PubMed-12728244; DOI=10.1038/sj.embor.embor930;
 RA Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;

THE MORTGAGE
REGISTRY

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Om protein - protein search, using sw model

Run on: March 30, 2006, 17:35:08 ; Search time 47 Seconds

Sequence: (without alignments) 184.701 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA,*

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 3: /cgn2_6/ptodata/1/iaa/H COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/PETUS COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 589 | 100.0 | 105 | 2 | US-09-712-529-5 |
| 2 | 589 | 100.0 | 105 | 2 | US-10-212-201A-5 |
| 3 | 589 | 100.0 | 105 | 2 | US-09-212-355-5 |
| 4 | 589 | 100.0 | 105 | 2 | US-09-931-181-371 |
| 5 | 589 | 100.0 | 105 | 2 | US-09-990-44-371 |
| 6 | 589 | 100.0 | 105 | 2 | US-09-997-333-371 |
| 7 | 589 | 100.0 | 105 | 2 | US-09-992-598-371 |
| 8 | 577 | 98.0 | 105 | 2 | US-09-621-976-350 |
| 9 | 448 | 76.1 | 80 | 2 | US-09-513-999C-4698 |
| 10 | 303 | 51.4 | 108 | 2 | US-09-712-529-2 |
| 11 | 303 | 51.4 | 108 | 2 | US-10-212-201A-2 |
| 12 | 303 | 51.4 | 108 | 2 | US-10-212-355-2 |
| 13 | 107.5 | 18.3 | 224 | 2 | US-09-161-241-14 |
| 14 | 102 | 17.3 | 186 | 2 | US-09-949-016-746 |
| 15 | 102 | 17.3 | 207 | 2 | US-09-161-241-13 |
| 16 | 102 | 17.3 | 259 | 2 | US-09-161-241-12 |
| 17 | 102 | 17.3 | 259 | 2 | US-09-949-016-6872 |
| 18 | 102 | 17.3 | 259 | 2 | US-10-012-231A-70 |
| 19 | 102 | 17.3 | 259 | 2 | US-10-015-389A-70 |
| 20 | 102 | 17.3 | 259 | 2 | US-10-006-768A-70 |
| 21 | 102 | 17.3 | 259 | 2 | US-10-015-671A-70 |
| 22 | 102 | 17.3 | 259 | 2 | US-10-015-393A-70 |
| 23 | 102 | 17.3 | 259 | 2 | US-10-011-833A-70 |
| 24 | 102 | 17.3 | 259 | 2 | US-10-006-041A-70 |
| 25 | 102 | 17.3 | 259 | 2 | US-10-012-064A-70 |
| 26 | 101 | 17.1 | 259 | 2 | US-09-161-241-11 |
| 27 | 100.5 | 17.1 | 259 | 2 | US-10-104-047-2196 |

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA,*

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 3: /cgn2_6/ptodata/1/iaa/H COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/PETUS COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 589 | 100.0 | 105 | 2 | US-09-712-529-5 |
| 2 | 589 | 100.0 | 105 | 2 | US-10-212-201A-5 |
| 3 | 589 | 100.0 | 105 | 2 | US-09-212-355-5 |
| 4 | 589 | 100.0 | 105 | 2 | US-09-931-181-371 |
| 5 | 589 | 100.0 | 105 | 2 | US-09-990-44-371 |
| 6 | 589 | 100.0 | 105 | 2 | US-09-997-333-371 |
| 7 | 589 | 100.0 | 105 | 2 | US-09-992-598-371 |
| 8 | 577 | 98.0 | 105 | 2 | US-09-621-976-350 |
| 9 | 448 | 76.1 | 80 | 2 | US-09-513-999C-4698 |
| 10 | 303 | 51.4 | 108 | 2 | US-09-712-529-2 |
| 11 | 303 | 51.4 | 108 | 2 | US-10-212-201A-2 |
| 12 | 303 | 51.4 | 108 | 2 | US-10-212-355-2 |
| 13 | 107.5 | 18.3 | 224 | 2 | US-09-161-241-14 |
| 14 | 102 | 17.3 | 186 | 2 | US-09-949-016-746 |
| 15 | 102 | 17.3 | 207 | 2 | US-09-161-241-13 |
| 16 | 102 | 17.3 | 259 | 2 | US-09-161-241-12 |
| 17 | 102 | 17.3 | 259 | 2 | US-09-949-016-6872 |
| 18 | 102 | 17.3 | 259 | 2 | US-10-012-231A-70 |
| 19 | 102 | 17.3 | 259 | 2 | US-10-015-389A-70 |
| 20 | 102 | 17.3 | 259 | 2 | US-10-006-768A-70 |
| 21 | 102 | 17.3 | 259 | 2 | US-10-015-671A-70 |
| 22 | 102 | 17.3 | 259 | 2 | US-10-015-393A-70 |
| 23 | 102 | 17.3 | 259 | 2 | US-10-011-833A-70 |
| 24 | 102 | 17.3 | 259 | 2 | US-10-006-041A-70 |
| 25 | 102 | 17.3 | 259 | 2 | US-10-012-064A-70 |
| 26 | 101 | 17.1 | 259 | 2 | US-09-161-241-11 |
| 27 | 100.5 | 17.1 | 259 | 2 | US-10-104-047-2196 |

Result 1
US-09-712-529-5
Sequence 5, Application US/09712529
Patent No. 648538
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/09/712.529
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows version 3.0
SEQ ID NO 5
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-712-529-5
RESULT 2
US-10-212-201A-5
Sequence 5, Application US/10212201A
Patent No. 6756479
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212.201A
CURRENT FILING DATE: 2002-08-02
PRIORITY APPLICATION NUMBER: US/09/712.529
PRIORITY FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SEQUENCE 9, Application US/09-161-241-9
Sequence 236, Application US/09-907-79A-236
Sequence 236, Application US/09-905-125A-236
Sequence 236, Application US/09-905-775A-236
Sequence 236, Application US/09-905-381A-236
Sequence 236, Application US/09-905-618A-236
Sequence 236, Application US/09-904-462A-236
Sequence 236, Application US/09-905-736A-236
Sequence 236, Application US/09-905-722A-236
Sequence 7856, Application US/09-948-016-7856
Sequence 7857, Application US/09-943-016-7857
Sequence 7858, Application US/09-949-016-7858
Sequence 8, Application US/09-161-241-8

; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-212-201A5

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 Best Local Similarity 100.0%; Pred. No. 1.2e-58;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRGATRVSIMLLVTVSDCAVITGACERVQCGAGTCCLISMRGLMCTPGRGEC 60

QY 61 HPGSHKVVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105
 Db 61 HPGSHKVVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 3
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; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-91
; CURRENT APPLICATION NUMBER: US/10/212,355
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Fast-SEQ for Windows - Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-212-355-5

Query Match 100.0%; Score 589; DB 2; Length 105;
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 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRGATRVSIMLLVTVSDCAVITGACERVQCGAGTCCLISMRGLMCTPGRGEC 60

QY 61 HPGSHKVVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105
 Db 61 HPGSHKVVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 4
 US-09-991-181-371
; Sequence 371, Application US/09991181
; Patent No. 6911919
; GENERAL INFORMATION:
; APPLICANT: Abkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Deaenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geurtsen, Mary E.
; APPLICANT: Goddard, Andrew
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Ivar J.

APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoli, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
; FILE REFERENCE: P2330P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065370
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/08322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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 PRIOR FILING DATE: 1998-07-09

Query Match: 100.0%; Score: 589; DB: 2; Length: 105;
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 Db 1 MRGATRVSMLAVTSDCAVTGACEDBVGAGTCACISWLRGLRNCCTPGLGEGEC 60
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RESULT 5
 US-09-990-444-371
 Sequence 371, Application US/09990444
 Patent No. 6930170
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritten, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavim, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2130PC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100%; Score 589; DB 2; Length 105;
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 ; GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
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 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hans-Peter
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 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumab, Daniel

APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2730P1C27
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; Query Match 100%; Score 589; DB 2; Length 105;
; Best Local Similarity 100.0%; Pred. No. 1.2e-58; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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; Sequence 371, Application US/0992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bottstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2710P1C20
CURRENT APPLICATION NUMBER: US/09/932,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-15
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-01-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
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PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858

PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
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PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25

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; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1; 2e-58; Mismatches 0; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-021-976-5350
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; Sequence 5350, Application US/09621976
; Patent No. 6633063
; GENERAL INFORMATION:
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 13335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105

Query Match          100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1; 2e-58; Mismatches 0; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Mine Edwards, J. B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59_592.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19.-1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: Seq VSIMLLVTVSDCAVITGACERDVQCGAGTCACISLWLRLGRNCTPLGREGSEC 60
; OTHER INFORMATION: US-09-513-999C-4698

Query Match          76.1%; Score 448; DB 2; Length 80;
Best Local Similarity 98.8%; Pred. No. 5; 8e-43; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 648938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-09-712-529-2

Query Match          51.4%; Score 303; DB 2; Length 108;
Best Local Similarity 55.2%; Pred. No. 1; 5e-26; Mismatches 24; Indels 0; Gaps 0;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
NAME/KEY: SIGNAL
LOCATION: -19.-1
NAME/KEY: UNSURE
LOCATION: 38
OTHER INFORMATION: Xaa = Ala, Gly
; OTHER INFORMATION: US-09-621-976-5350

Query Match          98.0%; Score 577; DB 2; Length 105;
Best Local Similarity 97.1%; Pred. No. 2; 7e-57; Mismatches 1; Indels 0; Gaps 0;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
NAME/KEY: UNSURE
LOCATION: 38
OTHER INFORMATION: Xaa = Ala, Gly
; OTHER INFORMATION: US-09-621-976-5350

Query Match          98.0%; Score 577; DB 2; Length 105;
Best Local Similarity 97.1%; Pred. No. 2; 7e-57; Mismatches 1; Indels 0; Gaps 0;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
NAME/KEY: UNSURE
LOCATION: 38
OTHER INFORMATION: Xaa = Ala, Gly
; OTHER INFORMATION: US-09-621-976-5350

Query Match          51.4%; Score 303; DB 2; Length 108;
Best Local Similarity 55.2%; Pred. No. 1; 5e-26; Mismatches 24; Indels 0; Gaps 0;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
NAME/KEY: UNSURE
LOCATION: 38
OTHER INFORMATION: Xaa = Ala, Gly
; OTHER INFORMATION: US-09-712-529-2

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RESULT 11
; Sequence 2, Application US/10212201A
; Patent No. 676479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Wittmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIORITY APPLICATION NUMBER: US/09/712,529
; PRIORITY FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-212-201A-2

Query Match      51.4%: Score 303; DB 2; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.5e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
Qy 10 MLLIVTVSDCAVITGACERDVGCGATCCASLWLRGLRMLCTPLGREGEECHGSSHKUPP 69
Db 18 LLUUPRAGDAAVITGACDKSPGGGMCCAVSIWKSIRICTPMGKUDSCHPLRKVPP 77
Qy 70 FRKKKHCTCPCLNLCLSRFPDRYRC 96
Db 78 FGRRMHHTCPCLPGLACLRTSFNRFC 104

RESULT 12
; Sequence 2, Application US/10212355
; Patent No. 6824425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Wittmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-212-355-2

Query Match      51.4%: Score 303; DB 2; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.5e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
Qy 10 MLLIVTVSDCAVITGACERDVGCGATCCASLWLRGLRMLCTPLGREGEECHGSSHKUPP 69
Db 18 LLUUPRAGDAAVITGACDKSPGGGMCCAVSIWKSIRICTPMGKUDSCHPLRKVPP 77
Qy 70 FRKKKHCTCPCLNLCLSRFPDRYRC 96
Db 78 FGRRMHHTCPCLPGLACLRTSFNRFC 104

RESULT 13
; Sequence 14, Application US/09161241
; Patent No. 634541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Dagang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
; US-09-161-241-14

Query Match      18.3%: Score 107.5; DB 2; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.00028;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;
Qy 25 AEBRDVOGAGTCCASLWLRGLRMLCTPLGREGEECHGSSHKUPPFRRKHKHTCPCLPNL 84
Db 144 SCURTFDGGPGLCCARHFW--TKICKPVLEGGQVCSRRGKUDQAPEIFQRCDCGPGL 200
Qy 85 IC 86
Db 201 LC 202

RESULT 14
; Sequence 7146, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7146
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7146

Query Match      17.3%: Score 102; DB 2; Length 186;
Best Local Similarity 31.5%; Pred. No. 0.00095;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;
Qy 26 CERDVOGAGTCCASLWLRGLRMLCTPLGREGEEC---HPSHKVPPFRKKHHTCPCL 81
Db 110 CIRASDCIEGFCRHRW--TKICKPVLEGGQVCSRRGKUDQAPEIFQRCDCGPGL 161

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Qy 82 PNLLCSRFPGRY 94
| : |
Db 162 KGLSCKWKD~~ATY~~ 174

RESULT 15

US-09-161-241-13 Application US/09161241

; Sequence 13, Application US/09161241

; Patent No. 6344541

; GENERAL INFORMATION:

; APPLICANT: Bass, Michael B

; APPLICANT: Sullivan, John K

; APPLICANT: Theill, Lars E

; APPLICANT: Wang, Deguang

; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES

; FILE REFERENCE: A-48

; CURRENT APPLICATION NUMBER: US/09/161,241

; CURRENT FILING DATE: 1996-09-25

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 207

; TYPE: PRT

; ORGANISM: Human

; US-09-161-241-13

Query Match 17.3%; Score 102; DB 2; Length 207;
Best Local Similarity 31.5%; Pred. No. 0.0011;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;
Qy 26 CERDVQCGAGTC~~CAISLWLRGLRMCTPLGREGBC---HPGSRKVPPFRKIRKHTC~~CL~~~~ 81
Db 131 CLASSDCIEGFCCARHFW--TKICKPVLHQEVCTKQRKKGS~~GLEIFOR-----CDCA~~ 182
Qy 82 PNLLCSRFPGRY 94
Db 183 KGLSCKWKD~~ATY~~ 195

Search completed: March 30, 2006, 17:36:29
Job time : 48 secs

PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
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 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
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 PRIOR FILING DATE: 1998-06-24
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 PRIOR FILING DATE: 1998-06-26
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 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. 1.4e-53; Mismatches 0; Indels 0; Gaps 0;
 Matches 105; Conservative

QY 1 MRGATRVSIMLLVTSACAVTGACERDVQGAGTCGCAISLWLRGLMCTPLGREGEC 60
 Db 1 MRGATRVSIMLLVTSACAVTGACERDVQGAGTCGCAISLWLRGLMCTPLGREGEC 60

QY 61 HPGSHKVPFRKRKGHTCOPCLPNLCSRFPDGYRCMSDLKINF 105
 Db 61 HPGSHKVPFRKRKGHTCOPCLPNLCSRFPDGYRCMSDLKINF 105

RESULT 3
 US-09-999-219-371
 Sequence 371, Application US/09989279
 Patent No. US20020072496A1
 GENERAL INFORMATION:
 APPLICANT: Askenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Devoeys, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferraro, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerbe, Hans Peter
 APPLICANT: Gerritzen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hane, Ivar J.
 APPLICANT: Kijavim, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Pao, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Thomas, Daniel
 APPLICANT: Wetanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PC56
 CURRENT APPLICATION NUMBER: US/09/989,279
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02

| | Matches | 105 | Conservative | 0 | Missmatches | 0 | Indels | 0 | Gaps | 0 |
|-------------------------------------|---------|-----------|--|----|-------------|--------|--------|---|------|---|
| PRIOR APPLICATION NUMBER: 60/089947 | Qy | 1 | MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCCTAISLWLRGLRMCTPLGREGBC | 60 | | | | | | |
| PRIOR FILING DATE: 1998-06-19 | Db | 1 | MRGATRVSIMLLVTVSDCAVITGACERDVQGAGTCCTAISLWLRGLRMCTPLGREGBC | 60 | | | | | | |
| PRIOR APPLICATION NUMBER: 60/089948 | Qy | 61 | HPGSHKVPFFRKRKHTCPCLPNLCSRFPDGRYRCMDLKNINF 105 | | | | | | | |
| PRIOR FILING DATE: 1998-06-19 | Db | 61 | HPGSHKVPFFRKRKHTCPCLPNLCSRFPDGRYRCMDLKNINF 105 | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/089952 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-06-22 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/089954 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-06-22 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/090349 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-06-23 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/090355 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-06-23 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/090429 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-06-24 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/090431 | | | | | | | | | | |
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| Best Local Similarity | 100.0% | Pred. No. | 1.48-53 | | | | | | | |

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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1; e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
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; Sequence 371, Application US/09991073
; Patent No. US20021227576A1
; GENERAL INFORMATION:
; APPLICANT: Askenzani, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bobstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferraro, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritzen, Mary E.
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Kjavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2130PC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
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Query Match: 100.0%; Score: 589; DB: 3; Length: 105;
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 Db 61 HPGSKVPPERKRKHTCCLPNLCSRPDGRCRSMDLNIF 105

RESULT 8
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 Sequence 371, Application US/09990442
 Patent No. US2002012252A1
 GENERAL INFORMATION:
 APPLICANT: Asbkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Boerstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Marty E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Roni, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tuma, Daniel
 APPLICANT: Wakana, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PC8
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 CURRENT FILING DATE: 2001-11-14
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Db 61 HPGSHKVPFFRKKHITCPCLPNLCSRFPGYRCMSDILKINF 105

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RESULT 10

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; Patent No. US2002137075A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bottstein, David
 APPLICANT: Desnoyers, Luc
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 APPLICANT: Williams, P. Mickey
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 APPLICANT: Zhang, Zemin
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; APPLICANT: Asbkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

RESULT 11
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

; RESULT 12
; US-09-982-721-371
; Sequence 371; Application US/09989721
; Patent No. US20030142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destroyer, Luc
; APPLICANT: Eaton, Dan L.

Query Match          100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Prod. No. 1.4e-53; Mismatches 0; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 HPGSHKVPFRKRKHTCPLPNLCSRPDGRTRCSMDLNKINP 105

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APPLICANT: Ferrara,Napolicone
APPLICANT: Fong,Sherman
APPLICANT: Gerber,Hanbapeiter
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Guirney,Austin L.
APPLICANT: Kjlavik,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy,Margaret Ann
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Wakanabe,Colin K.
APPLICANT: Williams,P. Mickey
APPLICANT: Wood,William T.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P-730p1C55
CURRENT APPLICATION NUMBER: US/09/9899,721
PRIOR APPLICATION NUMBER: 6/0/049787
PRIOR FILING DATE: 1997-05-16
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Query Match 100.0%; Score 589; DB 3; Length 105;
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RESULT 13
 US-09-992-598-371
 Sequence 371, Application US/09992598
 Patent No. US2000160384A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bottstein, David
 APPLICANT: Desnoyer, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
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 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acidic Encoding the Same
 FILE REFERENCE: P2730P1C20
 CURRENT APPLICATION NUMBER: US/09/992,598
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; Query Match
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; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2, Application US/09886242A
; Patient No. US2002172678A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Matanabe, Colin
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: EG-VEGF NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION AND METHODS OF USE
; FILE REFERENCE: GENENT-1516A
; CURRENT APPLICATION NUMBER: US/09-0886, 242A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/230, 978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/213, 637

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PRIOR FILING DATE: 2000-12-01
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PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
Remaining Prior Application data removed - See File Wrapper or PAML.
NUMBER OF SEQ ID NOS: 18
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LENGTH: 105
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ORGANISM: Homo sapiens
FEATURE: S-09-886-242A-2
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Destroyer, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Fong, Sherman
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APPLICANT: Williams, P. Mickey
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APPLICANT: Zhang, Zenii
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid
FILE REFERENCE: P27391C66
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; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/09178
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/09178
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

; Query Match 100.0%; Score 589; DB 3; length 105;
; Best Local Similarity 100.0%; Pred. 1.4e-53; Gaps 0;
; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 MRGATRVAIMLLVTVSDCAVITGACSHDVGAGTCATSIWLGLMCTFLGREGEC 60
; Db 1 MRGATRVAIMLLVTVSDCAVITGACSHDVGAGTCATSIWLGLMCTFLGREGEC 60
; Qy 61 HPGSHKVKPPRKHKHCPCLPNTLCSRDPDRYRCMSDLKINF 105
; Db 61 HPGSHKVKPPRKHKHCPCLPNTLCSRDPDRYRCMSDLKINF 105
; Qy 61 HPGSHKVKPPRKHKHCPCLPNTLCSRDPDRYRCMSDLKINF 105

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Search completed: March 30, 2006, 17:50:07
 Job time : 169 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model
Run on: March 30, 2006, 17:47:27 ; Search time 25 Seconds
(without alignments)
127.856 Million cell updates/sec

Title: US-10-692-299-2
Perfect score: 589

Sequence: 1 MRGATRVSIMLLVTVSDCA.....CSRFPFDGRTYRCSDLKNNIF 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /SIDS5/ptodata/1/pubpaasUS08_NEW_PUB_pep:*

2: /SIDS5/ptodata/1/pubpaasUS05_NEW_PUB_pep:*

3: /SIDS5/ptodata/1/pubpaasUS07_NEW_PUB_pep:*

4: /SIDS5/ptodata/1/pubpaasUS09_NEW_PUB_pep:*

5: /SIDS5/ptodata/1/pubpaasUS06_NEW_PUB_pep:*

6: /SIDS5/ptodata/1/pubpaasUS10_NEW_PUB_pep:*

7: /SIDS5/ptodata/1/pubpaasUS11_NEW_PUB_pep:*

8: /SIDS5/ptodata/1/pubpaasUS60__NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|--------------------------|-------------------|
| 1 | 589 | 100.0 | 105 6 US-10-131-826A-470 | Sequence 470, App |
| 2 | 589 | 100.0 | 105 6 US-10-973-115B-470 | Sequence 470, App |
| 3 | 588 | 99.8 | 105 6 US-10-475-075-194 | Sequence 194, App |
| 4 | 582 | 98.8 | 105 6 US-10-475-075-193 | Sequence 193, App |
| 5 | 582 | 98.8 | 105 6 US-10-475-075-477 | Sequence 477, App |
| 6 | 580 | 98.5 | 105 7 US-11-073-420-31 | Sequence 31, App |
| 7 | 572 | 97.1 | 105 7 US-11-073-420-28 | Sequence 28, App |
| 8 | 498 | 84.6 | 86 7 US-11-073-420-11 | Sequence 11, App |
| 9 | 455 | 77.2 | 86 7 US-11-073-420-12 | Sequence 12, App |
| 10 | 413 | 70.1 | 86 7 US-11-073-420-17 | Sequence 17, App |
| 11 | 376 | 63.8 | 81 7 US-11-073-420-16 | Sequence 16, App |
| 12 | 315 | 53.5 | 80 7 US-11-073-420-15 | Sequence 15, App |
| 13 | 300 | 50.9 | 108 7 US-11-073-420-6 | Sequence 6, App |
| 14 | 291 | 49.4 | 81 7 US-11-073-420-9 | Sequence 9, App |
| 15 | 286 | 48.6 | 80 7 US-11-073-420-10 | Sequence 10, App |
| 16 | 284 | 48.2 | 81 7 US-11-073-420-37 | Sequence 37, App |
| 17 | 267.5 | 45.4 | 77 7 US-11-073-420-14 | Sequence 14, App |
| 18 | 250.5 | 42.5 | 75 7 US-11-073-420-13 | Sequence 13, App |
| 19 | 107.5 | 18.3 | 224 7 US-11-255-790-5 | Sequence 5, App |
| 20 | 107.5 | 18.3 | 350 7 US-11-255-790-38 | Sequence 38, App |
| 21 | 102 | 17.3 | 179 7 US-11-255-790-11 | Sequence 11, App |
| 22 | 102 | 17.3 | 263 7 US-11-255-790-21 | Sequence 21, App |
| 23 | 101 | 17.1 | 272 7 US-11-255-790-36 | Sequence 36, App |
| 24 | 100.5 | 17.1 | 215 7 US-11-072-512-2196 | Sequence 216, App |
| 25 | 100.5 | 17.1 | 350 6 US-10-063-703-8 | Sequence 8, App |

ALIGNMENTS

| | |
|-------------------|-------------------|
| Sequence 8, App | Sequence 8, App |
| Sequence 2, App | Sequence 2, App |
| Sequence 17, App | Sequence 17, App |
| Sequence 428, App | Sequence 428, App |
| Sequence 428, App | Sequence 428, App |
| Sequence 5, App | Sequence 5, App |
| Sequence 212, App | Sequence 212, App |
| Sequence 211, App | Sequence 211, App |
| Sequence 4, App | Sequence 4, App |
| Sequence 6, App | Sequence 6, App |
| Sequence 213, App | Sequence 213, App |
| Sequence 10, App | Sequence 10, App |
| Sequence 25, App | Sequence 25, App |
| Sequence 16, App | Sequence 16, App |

Remaining Prior Application data removed - See File Wrapper or PALM.

Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2 5e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 470
 ORGANISM: Homo sapien
 US-10-131-826A-470

RESULT 2
 US-10-973-115B-470
 ; Sequence 470, Application US/10973115B
 ; Publication No. US20060040351A1
 GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Borensztein, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Elgaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritzen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Thomas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
 TITLE OF INVENTION: SAME
 FILE REFERENCE: 39870-330R1C300C1
 CURRENT APPLICATION NUMBER: US/10/973,115B
 CURRENT FILING DATE: 2004-10-22
 PRIOR APPLICATION NUMBER: US 10/145,747
 PRIOR FILING DATE: 2002-05-14
 PRIOR APPLICATION NUMBER: US 10/028,072
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: US 09/581,742
 PRIOR FILING DATE: 2000-06-16
 PRIOR APPLICATION NUMBER: PCT/US00/05746
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 60/135,736
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: US 60/123,090
 PRIOR FILING DATE: 1999-03-05
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO: 470
 LENGTH: 105
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-973-115B-470

Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2 5e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 193
 ORGANISM: Homo sapiens
 US-10-75-075-194
 ; Sequence 194, Application US/10475075
 ; Publication No. US2006053498A1
 GENERAL INFORMATION:
 ; APPLICANT: Belanin, Stephane
 ; APPLICANT: Tanka, Hiroaki
 ; APPLICANT: Dumas, Mine Edwards, Jean-Baptiste
 ; APPLICANT: Jobert, Severin
 ; APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
 FILE REFERENCE: G-081US03PCT
 CURRENT APPLICATION NUMBER: US/10/475,075
 CURRENT FILING DATE: 2003-10-17
 PRIOR APPLICATION NUMBER: PCT/IB01/00914
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 918
 SOFTWARE: Patent.pn
 SEQ ID NO: 194
 LENGTH: 105
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: -19 -1
 OTHER INFORMATION: Von Heijne matrix
 OTHER INFORMATION: score 7.2079835452081
 OTHER INFORMATION: seq VSTMALVTVSDCAV
 US-10-475-075-194

Query Match 99.8%; Score 588; DB 6; Length 105;
 Best Local Similarity 99.0%; Pred. No. 3.2e-56; Mismatches 0; Indels 0; Gaps 0;
 Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 61
 ORGANISM: Homo sapiens
 US-10-75-075-193
 ; Sequence 193, Application US/10475075
 ; Publication No. US2006053498A1
 GENERAL INFORMATION:
 ; APPLICANT: Belanin, Stephane
 ; APPLICANT: Tanka, Hiroaki
 ; APPLICANT: Dumas, Mine Edwards, Jean-Baptiste
 ; APPLICANT: Jobert, Severin
 ; APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
 FILE REFERENCE: G-081US03PCT
 CURRENT APPLICATION NUMBER: US/10/475,075
 CURRENT FILING DATE: 2003-10-17
 PRIOR APPLICATION NUMBER: PCT/IB01/00914
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 918
 SOFTWARE: Patent.pn
 LENGTH: 105
 TYPE: PRT
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: -19..-1
 OTHER INFORMATION: von Heijne matrix
 OTHER INFORMATION: score 7.20796835452081
 OTHER INFORMATION: seq VSIMLLIVTVSDC/AV
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 37..
 OTHER INFORMATION: xaa = Glu or *

US-10-475-075-193

Query Match

98.8%; Score 582; DB 6; Length 105;

Best Local Similarity 98.1%; Pred. No. 1.4e-55; Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

Db 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 5

US-10-475-075-477

Sequence 477, Application US/10475075

; Publication No. US200601053498A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins

FILE REFERENCE: G-081US03PCT

CURRENT APPLICATION NUMBER: US/10/475,075

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: PCT/IB01/00914

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 918

SOFTWARE: Patent.pm

SEQ ID NO 477

LENGTH: 105

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -19..-1

FEATURE:

NAME/KEY: UNSURE

LOCATION: 37..

OTHER INFORMATION: xaa = Lys or *

US-10-475-075-477

GENERAL INFORMATION:
 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 APPLICANT: Zhou, Qun-Yong
 TITLE OF INVENTION: Primate Prokineticin and Prokineticin
 TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods
 FILE REFERENCE: UCI1210-1
 CURRENT APPLICATION NUMBER: US/11/073,420
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 60/550,753
 PRIOR FILING DATE: 2004-03-05
 NUMBER OF SEQ ID NOS: 38

RESULT 6

US-11-073-420-11

Query Match 98.8%; Score 582; DB 6; Length 105;

Best Local Similarity 98.1%; Pred. No. 1.4e-55; Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

Db 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 6

US-11-073-420-31

Sequence 31, Application US/11073420

Publication No. US2006019338A1

GENERAL INFORMATION:
 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 APPLICANT: Zhou, Qun-Yong
 TITLE OF INVENTION: Primate Prokineticin and Prokineticin
 TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods
 FILE REFERENCE: UCI1210-1
 CURRENT APPLICATION NUMBER: US/11/073,420
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 60/550,753
 PRIOR FILING DATE: 2004-03-05
 NUMBER OF SEQ ID NOS: 38

RESULT 7

US-11-073-420-28

Query Match 98.5%; Score 580; DB 7; Length 105;

Best Local Similarity 98.1%; Pred. No. 2.3e-55; Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

Db 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 7

US-11-073-420-31

Query Match 98.8%; Score 582; DB 7; Length 105;

Best Local Similarity 97.1%; Pred. No. 1.6e-54; Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

Db 1 MRGATRVSIMLLIVTVSDCAVITGACERDVQGACTCCAIISLWLRGLRMCNTPLGREGEEC 60

QY 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

Db 61 HPGSHKVPFRKRKHTCPCLPNLCSRFDPGRYRCSDLKNINF 105

RESULT 8

US-11-073-420-11

Sequence 11, Application US/11073420

Publication No. US2006019338A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Zhou, Qun-Yong

TITLE OF INVENTION: Primate Prokineticin and Prokineticin

TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods

FILE REFERENCE: UC11210-1

CURRENT APPLICATION NUMBER: US/11/073,420

CURRENT FILING DATE: 2005-03-04

PRIOR APPLICATION NUMBER: 60/550,753

PRIOR FILING DATE: 2004-03-05

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO: 11

LENGTH: 86

TYPE: PRT

ORGANISM: Homo sapiens

US-11-073-420-11

RESULT 9

Query Match 84.6%; Score 498; DB 7; Length 86;

Best Local Similarity 100.0%; Pred. No. 1.2e-46; Mismatches 0; Indels 0; Gaps 0; Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 79

Db 1 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 60

QY 80 CLPNLILCSRFPDGRYRCMSDLQINP 105

Db 61 CLPNLILCSRFPDGRYRCMSDLQINP 86

US-11-073-420-12

Publication No. US2006019338A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Zhou, Qun-Yong

TITLE OF INVENTION: Primate Prokineticin and Prokineticin

FILE REFERENCE: UC11210-1

CURRENT APPLICATION NUMBER: US/11/073,420

CURRENT FILING DATE: 2005-03-04

PRIOR APPLICATION NUMBER: 60/550,753

PRIOR FILING DATE: 2004-03-05

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO: 12

LENGTH: 86

TYPE: PRT

ORGANISM: Mus musculus

US-11-073-420-12

Query Match 77.2%; Score 455; DB 7; Length 86;

Best Local Similarity 88.4%; Pred. No. 4.7e-42; Mismatches 5; Indels 0; Gaps 0; Matches 76; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 20 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 79

Db 1 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 60

QY 80 CLPNLILCSRFPDGRYRCMSDLQINP 105

Db 61 CLPNLILCSRFPDGRYRCMSDLQINP 86

US-11-073-420-16

Publication No. US2006019338A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Zhou, Qun-Yong

TITLE OF INVENTION: Primate Prokineticin and Prokineticin

FILE REFERENCE: UC11210-1

CURRENT APPLICATION NUMBER: US/11/073,420

CURRENT FILING DATE: 2005-03-04

PRIOR APPLICATION NUMBER: 60/550,753

PRIOR FILING DATE: 2004-03-05

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO: 16

LENGTH: 81

TYPE: PRT

ORGANISM: Homo sapiens

US-11-073-420-16

Query Match 63.8%; Score 376; DB 7; Length 81;

Best Local Similarity 84.4%; Pred. No. 1.3e-33; Mismatches 10; Indels 0; Gaps 0; Matches 65; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 20 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 79

Db 1 AVITGACERDVGAGTCGCAISLWLRGLRMTPLGREGEBCHPGSHKUFPFRKRKHTCP 60

QY 80 CLPNLILCSRFPDGRYRC 96

Db 61 CLPGLACRTSRNRFIC 77

US-11-073-420-15

Publication No. US2006019338A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Zhou, Qun-Yong

TITLE OF INVENTION: Primate Prokineticin and Prokineticin

TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods

FILE REFERENCE: UC11210-1

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